# Human-biting ticks and zoonotic tick-borne pathogens in North Africa: diversity, distribution, and trans-Mediterranean public health challenges

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A B S T R A C T

North Africa is home to more than 200 million people living across five developing economies (Egypt, Libya, Tunisia, Algeria, and Morocco) and two Spanish exclaves (Ceuta and Melilla), many of whom are impacted by ticks and tick-borne zoonoses. Populations in Europe are also increasingly vulnerable to North African ticks and tick-borne zoonoses due to a combination of climate change and the movement of ticks across the Mediterranean on migratory birds, human travellers, and trafficked wildlife. The human-biting ticks and tick-borne zoonoses in North Africa are reviewed along with their distribution in the region. We also assess present and future challenges associated with ticks and tick-borne zoonoses in North African and highlight opportunities for collaboration and coordination between governments in Europe and North Africa to address public health challenges posed by North African ticks and tick-borne zoonoses.

## 1. Introduction

Ticks represent a major threat to public health worldwide, due to their ability to transmit numerous zoonoses. In addition, tick bites can induce paralysis and allergic reactions [1–5]. Tick-borne pathogens are maintained in tick-vertebrate cycles, causing morbidity and mortality when they spillover to humans [6]. In recent decades, ticks and tick-borne diseases have experienced shifting geographic ranges, due to urbanization, increased global trade and travel, changes in land use, and climate changes, resulting in changing rates of exposure to ticks and tick-borne zoonoses [7].

The North African region (herein defined as Egypt, Libya, Tunisia, Algeria, Morocco, Ceuta, and Melilla) stretching from the Atlantic Ocean in the west to the Red Sea and Suez Canal to the East is bordered by the Mediterranean Sea in the north, and the Sahara Desert in the south. Being an important source of energy, minerals, and other resources, as well as a major transportation hub, North African region is important to the global economy. While each North African country has a unique range of geographic features, varying from the Atlas mountain ranges in northern Morocco, Algeria, and Tunisia to the arid deserts of southern North Africa, they share a Mediterranean climate with four seasons characterised by hot and dry summers and cool and wet winters [8,9].

These ecological and climatic conditions support a rich diversity of tick species and tick-borne pathogens in North Africa. The proximity of North Africa to south Europe to the north and sub-Saharan Africa to the south, means that ticks from these two regions also have the potential to be transported into and out of North Africa through migratory birds, traded animals (livestock and exotic pets), and on human travellers.

Knowledge of human-biting ticks and tick-borne zoonoses in North Africa is patchy and scattered across numerous publications [10]. This imposes significant challenges on public health officials and clinicians trying to ascertain a clear idea of the distribution and risks associated with particular ticks or zoonotic pathogens in North Africa. To address this challenge, we review the diversity of human-biting ticks and zoonotic tick-borne pathogens present in North Africa and their distribution across the region. We also assess the present and future challenges associated with the surveillance and control of ticks and tick-borne zoonoses in North Africa.

## 2. Tick-borne zoonoses of North Africa

In North Africa, numerous tick-borne zoonoses have been recorded including anaplasmosis, borreliosis, ehrlichiosis, Q fever, tick-borne rickettsiosis, babesiosis, Alkhurma hemorrhagic fever, Crimean Congo-

hemorrhagic fever, and tick-borne encephalitis (Table 1). Additionally, DNA/RNA from a wide range of zoonotic pathogens has been detected in numerous local tick genera including *Rhipicephalus, Hyalomma, Ixodes, Haemaphysalis, Dermacentor, Argas,* and *Ornithodoros* (Table 2).

## 2.1. Bacterial diseases

### 2.1.1. Anaplasmosis

Human anaplasmosis or human granulocytic anaplasmosis is an emerging tick-borne disease caused by the gram-negative bacterium *Anaplasma phagocytophilum*. This bacterium is primarily transmitted to humans through the bites of *Ixodes* ticks [180]. Other modes of transmission, however, have been described, including transplacental transmission, percutaneous exposure or inhalation of contaminated blood, nosocomial infection following direct contact with blood and respiratory secretions, and blood transfusion [181].

Human granulocytic anaplasmosis manifests as an acute fever, chills, malaise, myalgia, nausea, and coughing. The infection can range from mild to fatal, depending on several risk factors such as the patient's age, immunosuppression, co-morbidities, and treatment delays [180,181]. Approximately 36% of cases require hospitalization, but most patients recover without complications and the case fatality rate is low (< 1%) [180]. Additionally, *A. phagocytophilum* is the leading cause of tick-borne fever in ruminants, canine, and equine, which have a significant economic impact due to reduced growth, abortion, or animal losses [182].

In Algeria, *A. phagocytophilum* was identified among apparently healthy and diseased camels (22.5%/80), dogs (47.4%/213), cattle (41.7%/36), and horses (19.5%/128) [15,17,20,22], as well as *Argas persicus* ticks [130]. In Tunisia, circulation of antibodies against *A. phagocytophilum* was reported in camels (29.2%/226) and molecularly confirmed in cattle (0.6%/328) [183], dogs (2%/268) [21], horses (13%/60) [24], small ruminants (sheep and goats) (11.3%/257) [25], and ticks (*Ixodes ricinus, Hyalomma egyptium, Hyalomma detrium,* and *Hyalomma marginatum*) [24,133,134]. In Egypt, *A. phagocytophilum* was recorded in a symptomatic humans in contact with sheep (5.6%/18) and farmers (8.96%/67) [11,12]. Additionally, *A. phagocytophilum* infection was reported in sheep (10%/30) [11] and ticks (*Rh. sanguinius* and *Hyalomma anatolicum excavatum*) [131,132].

In Morocco, human exposure to *A. phagocytophilum* was serologically detected among blood donors (22%/117) [13] as well as dog owners (70%/10, and 27%/144) [13,14]. In addition to *A. phagocytophilum,* a novel emerging zoonotic *Anaplasma capra* was isolated from cattle (28.8%/257, and 11.3%/257, respectively) [18]. *Anaplasma capra* was reported from Chinese patients in 2015 [184]. Thus far, *A. capra* has been isolated from humans, cattle, sheep, buffalo, dogs, and wild animals in different countries belonging to Africa, Asia, and Europe [185].

### 2.1.2. Borreliosis

#### 2.1.2.1. Lyme disease.
Lyme disease is a bacterial tick-borne infection, primarily caused by *Borrelia burgdorferi* in North America and *Borrelia garinii* or *Borrelia afzelii* in Asia and Europe. Further *Borrelia* species such as *Borrelia lusitaniae* and *Borrelia valaisiana* have been infrequently detected in patients [7]. Infection typically commences with an erythema migrans rash, which if left untreated can lead to early disseminated infection, manifested by neurological abnormalities, arthritis, dermatitis, or carditis [186].

In Morocco, two cases of Lyme disease were diagnosed in two Moroccan patients in whom the disease was manifested by facial paralysis [187]. Furthermore, *B. burgdorferi, B. lusitaniae, B. garinii,* and *B. valaisiana* were isolated from *I. ricinus* in North Africa [136,188]. In Algeria, acute encephalitis of *B. burgdorferi* was reported in an Algerian child suffering from renal insufficiency [27] and a serosurvey of *B. burgdorferi* among blood donors, foresters, and breeders detected

infection rate of 1.1% among 874 tested [26]. Additionally, *B. burgdorferi* antibodies were detected from dogs (37.6%/213) and horses (21.8%/128) [20,22].

In Tunisia, 29 patients (10.7%/271) diagnosed with Lyme borreliosis had neurological and articular signs [29]. *Borrelia* DNA was isolated from camels (1.8%/226), cattle (1.3%/232), sheep (6.2%/260), and goats (30.4%/303) [30]. Furthermore, *B. lusitaniae* was molecularly identified in *Psammodromus algirus* lizards (21.8%/78) [33]. In addition to *B. lusitaniae, B. burgdorferi, B. garinii,* and *B. valaisiana* were identified in *I. ricinus* [33,138,139,188].

In Egypt, *B. burgdorferi* was isolated from farmers (26.6%/15) and humans with acute febrile illness (3%/67) who were in contact with feverish dogs and cattle [12,28]. *Borrelia burgdorferi* DNA has been isolated from dogs, cattle, and their attached ticks (*Rhipicephalus sanguineus* and *Hy. anatolicum excavatum*) [28,31]. Additionally, seroprevalence of *B. burgdorferi* was 1.9% (9/500) in pet dogs [32].

#### 2.1.2.2. Tick-borne relapsing fever (TBRF).
Tick-borne relapsing fever (TBRF) is a bacterial illness manifesting as recurring bouts of fever, caused by relapse fever group *Borrelia* (e.g., *Borrelia duttonii, Borrelia hispanica, Borrelia persica, Borrelia crocidurae, Borrelia turicatae,* and *Borrelia parkeri*). The infection is transmitted to humans through the bites of infected *Ornithodoros* ticks. TBRF is frequently misdiagnosed, and its true prevalence is greatly underestimated. The disease is uncommon in North Africa, but it is endemic in Sub-Saharan Africa, where the most common *Borrelia* species are *B. crocidurae* and *B. duttonii* [189].

In Algeria, *Borrelia algerica* was isolated from a febrile patient (0.39%/257) [34]. Other *Borrelia* species including *B. hispanica, B. turicatae, B. turcica,* and *B. crocidurae* were identified in *Ornithodoros capensis, Hyalomma aegyptium,* and *Ornithodoros* sp. [140,144,145]. In Morocco, 26 febrile patients (20.5%/127) living in Kenitra were diagnosed with *B. hispanica* relapsing fever, manifesting with fever, chills, myalgia, and gastrointestinal disorders [35]. In another survey, *Borrelia* was reported among Moroccan patients (99/89995) and rodents (12/140) [39]. *Borrelia hispanica* infection was identified in a 13-year-old Moroccan girl presented with abdominal cramps and high fever. Among travellers, *B. hispanica* relapsing fever was detected in a 20-year-old New Zealand woman who had recurrent episodes of fever and meningitis, after a holiday in Morocco [37]. Similarly, infection with *B. hispanica* was reported in a French traveller who developed recurrent flu-like symptoms, myalgia and arthritis, after a trip in Morocco [38]. Additionally, *B. crocidurae, B. hispanica,* and *B. merionesi* were isolated from *Ornithodoros* ticks [39,140,142,143]. In Tunisia, *B. crocidurae* was also detected in *Ornithodoros* ticks [140,141].

### 2.1.3. Ehrlichiosis

Human ehrlichiosis is an emerging tick-borne zoonosis, caused by the intracellular, gram-negative bacterium, belonging to the genus *Ehrlichia*. The two main agents of human ehrlichiosis are *Ehrlichia chaffeensis* and *Ehrlichia ewingii*, causing human monocytic ehrlichiosis and *E. ewingii* ehrlichiosis, respectively [190]. Most reported cases are from the USA where the tick vector *Amblyomma americanum* is implicated in transmission. The clinical spectra of the disease in humans range from asymptomatic to mild febrile symptoms. However, immunocompromised patients are at greatest risk of developing complications of ehrlichiosis, including prolonged fever, coagulopathy, adult respiratory distress syndrome, and neurological manifestations [191]. In Tunisia, *E. ewingii* was identified in one *Atelerix algirus* hedgehog and *Haemaphysalis erinacei* ticks, using molecular tools [40]. Likewise, *E. ewingii* was detected in *Hy. aegyptium* ticks collected from Algerian tortoises imported to Italy [146].

### 2.1.4. Q fever

Q fever is a ubiquitous zoonosis caused by an intracellular gram-negative bacterium, *Coxiella burnetii,* which has a worldwide

**Table 1**
Summary of current knowledge on zoonotic tick-borne pathogens in North Africa detected in humans or animals.

| Tick-borne zoonosis | Pathogen | Host(s) | Country | No. investigated | Prevalence (%) | Detection method(s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|---|---|
| Anaplasmosis | *Anaplasma phagocytophilum* | *Homo sapiens* | Egypt | 18 | 5.6 | Nested PCR | 16S rRNA | [11] |
| | *Anaplasma phagocytophilum* | *Homo sapiens* | Egypt | 67 | 9 | Nested PCR | 16S rRNA | [12] |
| | *Anaplasma phagocytophilum* | *Homo sapiens* | Morocco | 144 | 27 | IFAT | | [13] |
| | *Anaplasma phagocytophilum* | *Homo sapiens* | Morocco | 117 | 22 | IFAT | | [13] |
| | *Anaplasma phagocytophilum* | *Homo sapiens* | Morocco | 10 | 70 | IFAT | | [14] |
| | *Anaplasma phagocytophilum* | *Camelus dromedarius* | Algeria | 80 | 22.5 | PCR, sequencing | 23S rRNA | [15] |
| | *Anaplasma phagocytophilum* | *Camelus dromedarius* | Tunisia | 226 | 29.2 | IFAT | | [16] |
| | *Anaplasma phagocytophilum* | *Bos taurus* | Algeria | 36 | 41.7 | PCR, sequencing | 23S rRNA | [17] |
| | *Anaplasma phagocytophilum* | *Bos taurus* | Morocco | 257 | 28.8 | PCR, sequencing | 16S rRNA | [18] |
| | *Anaplasma phagocytophilum* | *Bos taurus* | Tunisia | 328 | 0.6 | Duplex PCR | *msp*2, *msp*4 | [19] |
| | *Anaplasma phagocytophilum* | *Canis familiaris* | Algeria | 213 | 47.4 / 0 | IFAT / PCR, sequencing | | [20] |
| | *Anaplasma phagocytophilum* | *Canis familiaris* | Tunisia | 286 | 25.5 / 2 | IFAT / RLB | | [21] |
| | *Anaplasma phagocytophilum* | *Equus ferus* | Algeria | 128 | 19.5 / 25.9 | IFAT / ELISA | | [22] |
| | *Anaplasma phagocytophilum* | *Equus ferus* | Tunisia | 343 | 16.3 | IFAT | | [23] |
| | *Anaplasma phagocytophilum* | *Equus ferus* | Tunisia | 60 | 67 / 13 | IFAT / Nested PCR | 16S rRNA | [24] |
| | *Anaplasma phagocytophilum* | *Ovis aries* | Egypt | 30 | 10 | Nested PCR | 16S rRNA | [11] |
| | *Anaplasma phagocytophilum* | *Ovis aries, Capra hircus* | Tunisia | 263 | 5.7 | Duplex PCR | *msp2* | [25] |
| | *Anaplasma capra* | *Bos taurus* | Morocco | 257 | 11.3 | PCR, sequencing | 16S rRNA | [18] |
| Borreliosis | *Borrelia burgdorferi* | *Homo sapiens* | Algeria | 874 | 1.1 | ELISA, Western blot | | [26] |
| | *Borrelia burgdorferi* | *Homo sapiens* | Algeria | 1 | | Serology | | [27] |
| | *Borrelia burgdorferi* | *Homo sapiens* | Egypt | 15 | 26.6 | ELISA, PCR, sequencing | *ospA* | [28] |
| | *Borrelia burgdorferi* | *Homo sapiens* | Egypt | 67 | 3 | PCR | *ospA* | [12] |
| | *Borrelia burgdorferi* | *Homo sapiens* | Tunisia | 271 | 10.7 | ELISA | | [29] |
| | *Borrelia burgdorferi* | *Camelus dromedarius* | Tunisia | 226 | 1.8 | qPCR | 23S rRNA | [30] |
| | *Borrelia burgdorferi* | *Bos taurus* | Egypt | 25 | 16 | Culturing, PCR, sequencing | *ospA* | [28] |
| | *Borrelia burgdorferi* | *Bos taurus* | Tunisia | 232 | 1.3 | qPCR | 23S rRNA | [30] |
| | *Borrelia burgdorferi* | *Canis familiaris* | Egypt | 26 | 23 | PCR, sequencing | *ospA* | [28] |
| | *Borrelia burgdorferi* | *Canis familiaris* | Egypt | 100 | 1 | PCR, sequencing | 16S rRNA | [31] |
| | *Borrelia burgdorferi* | *Canis familiaris* | Egypt | 500 | 1.8 | ELISA | | [32] |
| | *Borrelia burgdorferi* | *Canis familiaris* | Algeria | 213 | 37.6 | IFAT | | [20] |
| | *Borrelia burgdorferi* | *Capra hircus* | Tunisia | 303 | 30.4 | qPCR | 23S rRNA | [30] |
| | *Borrelia burgdorferi* | *Equus ferus* | Algeria | 128 | 21.8 / 14.8 | IFAT / ELISA | | [22] |
| | *Borrelia burgdorferi* | *Ovis aries* | Tunisia | 260 | 6.2 | qPCR | 23S rRNA | [30] |
| | *Borrelia lusitanae* | *Psammodromus algirus* | Tunisia | 78 | 21.8 | Culturing, PCR, PCR-RFLP | 5S–23S rRNA spacer | [33] |
| | *Borrelia algerica* | *Homo sapiens* | Algeria | 257 | 0.4 | PCR | *flaB* | [34] |
| | *Borrelia hispanica* | *Homo sapiens* | Morocco | 127 | 20.5 | Nested PCR | 16S-23S rRNA spacer, 16S rRNA | [35] |
| | *Borrelia hispanica* | *Homo sapiens* | Morocco | 1 | | PCR | 16S rRNA | [36] |
| | *Borrelia hispanica* | *Homo sapiens* | Morocco | 1 | | PCR | 16S rRNA | [37] |
| | *Borrelia hispanica* | *Homo sapiens* | Morocco | 1 | | PCR | 16S rRNA | [38] |
| | *Borrelia* spp. | *Homo sapiens* | Morocco | 89995 | 0.1 | Blood film | | [39] |
| Ehrlichiosis | *Ehrlichia ewingii* | *Atelerix algirus* | Tunisia | 20 | 5 | PCR, nested PCR, qPCR, sequencing | 16S rRNA | [40] |
| Q fever | *Coxiella burnetii* | *Homo sapiens* | Algeria | 729 | 15.5 | IFAT | | [41] |
| | *Coxiella burnetii* | *Homo sapiens* | Algeria | 108 | 1.9 | IFAT, nested PCR | *IS*1111 | [42] |
| | *Coxiella burnetii* | *Homo sapiens* | Algeria | 1 | | IFAT | | [43] |
| | *Coxiella burnetii* | *Homo sapiens* | Algeria | 380 | 0.8 | IFAT, qPCR | *IS*30, *IS*1111 | [44] |
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 54 | 5.6 | PCR | *IS*1111 | [45] |
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 63 | 1.6 | IFAT | | [46] |
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 133 | 1.5 | IFAT | | [47] |
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 120 | 37.5 | IFAT, ELISA, PCR | *IS*1111 | [48] |
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 418 | 32 | ELISA | | [49] |

**Table 1** (*continued*)

| Tick-borne zoonosis | Pathogen | Host(s) | Country | No. investigated | Prevalence (%) | Detection method(s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|---|---|
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 58 | 19 | ELISA | *IS111* | [50] |
| | *Coxiella burnetii* | *Homo sapiens* | Egypt | 35 | 25.7 | ELISA | | [51] |
| | *Coxiella burnetii* | *Homo sapiens* | Morocco | 426 | 6.1 | IFAT | | [52] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 500 | 26 | IFAT | | [53] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 47 | 8.5 | IFAT, Western blot | | [54] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 21 | | IFAT | | [55] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 1 | | qPCR, PCR, genome sequencing | Cox2, Cox5, Cox18, Cox20, Cox22, Cox 37, Cox51, Cox56, Cox57, Cox61 | [56] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 1 | | Serology¶ | | [57] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 300 | 2 | IFAT, ELISA | | [58] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 1 | | Serology¶, PCR | | [59] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 1 | | ELISA | | [60] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia | 240 | 6.6 | Serology¶ | | [61] |
| | *Coxiella burnetii* | *Homo sapiens* | Tunisia, Algeria, Morocco | 1888 | 0.1 | PCR, qPCR, sequencing | *IS30, IS1111* | [62] |
| | *Coxiella burnetii* | *Atelerix algirus* | Algeria | 21 | 42.9 | qPCR, sequencing | *IS30A, IS1111, gltA, Sca*1 | [63] |
| | *Coxiella burnetii* | *Atelerix algirus* | Tunisia | 20 | 10 | PCR, nested PCR, qPCR sequencing | 16S rRNA | [40] |
| | *Coxiella burnetii* | *Bos taurus* | Algeria | 77 | 19.1 | qPCR, PCR, sequencing, | *IS1111, IS30A*, Cox2, Cox5, Cox18, Cox37, Cox56, Cox57, Cox61 | [64] |
| | *Coxiella burnetii* | *Bos taurus* | Algeria | 368 | 8.4 | ELISA | | [65] |
| | *Coxiella burnetii* | *Bos taurus* | Algeria | 360 | 1.7 | ELISA | | [66] |
| | *Coxiella burnetii* | *Bos taurus* | Algeria | 186 | 6.9 | ELISA, PCR, sequencing | *IS1111* | [67] |
| | *Coxiella burnetii* | *Bos taurus* | Algeria | 678 | 11.4 | ELISA | | [68] |
| | *Coxiella burnetii* | *Bos taurus* | Egypt | 840 | 19.3 | ELISA | | [69] |
| | *Coxiella burnetii* | *Bos taurus* | Egypt | 1194 | 13.2 | ELISA | | [70] |
| | *Coxiella burnetii* | *Bos taurus, Bubalus bubalis, Capra hircus, Ovis aries* | Egypt | 108 | 0.9 | ELISA, nested PCR, sequencing | *IS111* | [50] |
| | *Coxiella burnetii* | *Bos taurus, Capra hircus, Ovis aries* | Egypt | 160 | 21.3 | IFAT, ELISA, qPCR | *IS111* | [48] |
| | *Coxiella burnetii* | *Bubalus bubalis* | Egypt | 304 | 11.2 | ELISA | | [69] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Algeria | 184 | 75.5 | ELISA, qPCR, sequencing | *IS1111, htpB* | [71] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Algeria | 184 | 71.2 | ELISA | | [72] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Algeria | 184 | 75.5 | ELISA | | [71] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Egypt | 528 | 40.7 | ELISA | | [69] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Egypt | 315 | 22 | ELISA | | [73] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Egypt | 112 | 16.9 | ELISA, PCR | SOD | [74] |
| | *Coxiella burnetii* | *Camelus dromedarius* | Tunisia | 534 | 44 | ELISA | | [75] |
| | *Coxiella burnetii* | *Canis familiaris, Felis catus* | Algeria | 224 | 0.9 | qPCR | *IS30, IS1111* | [76] |
| | *Coxiella burnetii* | *Canis familiaris* | Egypt | 48 | 0 | Nested PCR, sequencing | *IS111* | [77] |
| | *Coxiella burnetii* | *Capra hircus, Ovis aries* | Algeria | 267 | 21.3 | ELISA, qPCR | *IS1111* | [78] |
| | *Coxiella burnetii* | *Capra hircus, Ovis aries* | Algeria | 150 | 75.3 | ELISA | | [79]* |
| | *Coxiella burnetii* | *Capra hircus* | Egypt | 311 | 6.8 | ELISA | | [69] |
| | *Coxiella burnetii* | *Capra hircus, Ovis aries* | Egypt | 284 | 15.5 | ELISA | | [80] |
| | *Coxiella burnetii* | *Capra hircus, Ovis aries* | Morocco | 23 | 57 | ELISA | | [81]* |
| | *Coxiella burnetii* | *Capra hircus, Ovis aries* | Tunisia | 253 | 19.4 | Multiplex PCR, ELISA | *IS1111* | [82] |
| | *Coxiella burnetii* | *Capra hircus, Ovis aries* | Egypt | 91 | 2.2 | PCR, qPCR, sequencing | *IS1111*, Cox2, Cox5, Cox18 | [83] |
| | *Coxiella burnetii* | *Capra hircus* | Egypt | 39 | 28.2 | ELISA | | [51] |
| | *Coxiella burnetii* | *Capra hircus* | Egypt | 80 | 16.3 | ELISA, qPCR | *gltA* | [84] |
| | *Coxiella burnetii* | *Felis catus* | Egypt | 40 | 7.5 | Nested PCR, sequencing | *IS111* | [77] |
| | *Coxiella burnetii* | *Ovis aries* | Algeria | 226 | 12.4 | ELISA | | [85] |
| | *Coxiella burnetii* | *Ovis aries* | Algeria | 184 | 24.9 | ELISA | | [86] |
| | *Coxiella burnetii* | *Ovis aries* | Egypt | 716 | 8.9 | ELISA | | [69] |
| | *Coxiella burnetii* | *Ovis aries* | Egypt | 109 | 5.7 | ELISA | | [51] |
| | *Coxiella burnetii* | *Ovis aries* | Egypt | 110 | 33.6 | ELISA, qPCR | *gltA* | [84] |
| | *Coxiella burnetii* | *Ovis aries* | Tunisia | 492 | 11.8 | qPCR assay, ELISA | *IS1111* | [87] |
| | *Coxiella burnetii* | *Rattus norvegicus, Rattus rattus* | Egypt | 75 | 6.7 | Nested PCR, sequencing | *IS1111* | [88] |

(*continued on next page*)

**Table 1** (*continued*)

| Tick-borne zoonosis | Pathogen | Host(s) | Country | No. investigated | Prevalence (%) | Detection method(s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|---|---|
| Tick-borne rickettsiosis | *Rickettsia conorii* | *Homo sapiens* | Algeria | 24 | | IFAT, Western blot | | [89] |
| | *Rickettsia conorii conorii* | *Homo sapiens* | Algeria | 39 | 64 | qPCR | RC0338 | [90] |
| | *Rickettsia conorii conorii* | *Homo sapiens* | Algeria | 93 | 57 | IFAT, Western blot | | [91] |
| | *Rickettsia conorii conorii* | *Homo sapiens* | Algeria | 167 | | IFAT, Western blot, PCR, sequencing | *ompA* | [92] |
| | *Rickettsia conorii* | *Homo sapiens* | Algeria | 22 | | PCR, sequencing, multispacer typing | *gltA, ompA* | [93] |
| | *Rickettsia conorii conorii* | *Homo sapiens* | Algeria | 108 | 4.6 | IFAT, Western blot | | [94] |
| | *Rickettsia conorii* | *Homo sapiens* | Algeria | 166 | 34.3 | IFAT, qPCR | *gltA* | [95] |
| | *Rickettsia conorii* | *Homo sapiens* | Algeria | 34 | | IFAT | | [96] |
| | *Rickettsia conorii* | *Homo sapiens* | Egypt | 371 | 37 | ELISA | | [49] |
| | *Rickettsia conorii* | *Homo sapiens* | Egypt | 178 | 1 | IFAT | | [97] |
| | *Rickettsia conorii* | *Homo sapiens* | Libya | 1 | | IFAT | | [98] |
| | *Rickettsia conorii* | *Homo sapiens* | Morocco | 1 | | IFAT | | [99] |
| | *Rickettsia conorii* | *Homo sapiens* | Morocco | 426 | 6.6 | IFAT | | [52] |
| | *R. conorii conorii* | *Homo sapiens* | Morocco | 45 | 46.7 | Serology¶, Western blot, PCR, sequencing | *gltA, ompA* | [100] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 638 | 0.5 | IFAT, Western blot | | [101] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 101 | 47.5 | qPCR, RLB | 5S-23SrRNA spacer | [102] |
| | *R. conorii conorii.* | *Homo sapiens* | Tunisia | 25 | | IFAT, PCR, sequencing | *gltA, ompA* | [103] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 200 | | IFAT | | [104] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 30 | | IFAT | | [105] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 500 | 9 | IFAT, Western blot | | [53] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 300 | 22.6 | IFAT, ELISA | | [58] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 35 | 57.1 | Serology¶ | | [106] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 47 | 15 | IFAT, Western blot | | [54] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 119 | 52.1 | IFAT, Western blot | | [107] |
| | *Rickettsia conorii* | *Homo sapiens* | Tunisia | 80 | | IFAT | | [108] |
| | *Rickettsia conorii* | *Rattus rattus* | Egypt | 82 | 4 | IFAT | | [109] |
| | *Rickettsia conorii israelensis* | *Homo sapiens* | Tunisia | 25 | 12 | IFAT, PCR, sequencing | *gltA, ompA, ompB* | [103] |
| | *Rickettsia conorii israelensis* | *Homo sapiens* | Tunisia | 2 | | IFAT, PCR, sequencing | *ompA, ompB* | [110] |
| | *Rickettsia aeschlimannii* | *Homo sapiens* | Algeria | 2 | | IFAT, Western blot, cross-adsorption assays | | [111] |
| | *Rickettsia aeschlimannii* | *Homo sapiens* | Morocco | 1 | | IFAT, Western blot, PCR, sequencing | *ompA,* | [112] |
| | *Rickettsia aeschlimannii* | *Homo sapiens* | Tunisia | 638 | 0.3 | IFAT, Western blot | | [101] |
| | *Rickettsia aeschlimannii,* | *Camelus dromedarius* | Tunisia | 293 | 0.7 | Nested PCR, sequencing | *ompA, ompB* | [113] |
| | *Rickettsia aeschlimannii* | *Rattus rattus, Meriones shawi* | Tunisia | ND | ND | PCR, sequencing | *ompB, ompA* | [114] |
| | *Rickettsia sibirica mongolitimonae* | *Homo sapiens* | Egypt | 1 | | IFAT, Western blot, PCR, sequencing | *gltA, ompA, ompB* | [115] |
| | *Rickettsia massiliae* | *Rattus rattus, Meriones shawi* | Tunisia | ND | ND | PCR, sequencing | *ompB, gltA* | [114] |
| | *Rickettsia massiliae* | *Camelus dromedarius* | Tunisia | 293 | 0.3 | Nested PCR, sequencing | *ompA, ompB* | [113] |
| | *Rickettsia massiliae* | *Homo sapiens* | Tunisia | 101 | 1 | qPCR, RLB | 5S-23S rRNA spacer | [102] |
| | *Rickettsia slovaca* | *Sus scrofa algira* | Algeria | 92 | 5.4 | qPCR, sequencing | *gltA, ompA* | [116] |
| | *Rickettsia monacensis* | *Rattus rattus, Meriones shawi* | Tunisia | ND | ND | PCR, sequencing | *ompB, ompA, gltA* | [114] |
| | *Rickettsia helvetica,* | *Rattus rattus, Meriones shawi* | Tunisia | | | PCR, sequencing | *ompB,* | [114] |
| | *Rickettsia helvetica* | *Camelus dromedarius* | Tunisia | 293 | 0.3 | Nested PCR, sequencing | *ompA, ompB* | [113] |
| | *Rickettsia africae* | *Rattus rattus, Meriones shawi* | Tunisia | ND | ND | PCR, sequencing | *ompB,* | [114] |
| | *Rickettsia monacensis* | *Camelus dromedarius* | Tunisia | 293 | 1.4 | Nested PCR, sequencing | *ompA, ompB* | [113] |
| | *Rickettsia* spp. | *Homo sapiens* | Tunisia | 77 | 24.7 | IFAT, duplex qPCR | ND | [117] |
| Babesiosis | *Babesia divergens* | *Bos taurus* | Tunisia | 1 | | Animal inoculation, blood smear | | [118] |
| | *Babesia divergens* | *Bos taurus* | Tunisia | 307 | 44.6 | IFAT, animal inoculation | | [119] |

**Table 1** (*continued*)

| Tick-borne zoonosis | Pathogen | Host(s) | Country | No. investigated | Prevalence (%) | Detection method(s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|---|---|
| Alkhurma hemorrhagic fever | AHF virus | *Homo sapiens* | Egypt | 2 | | ELISA, IFAT, reverse transcription-PCR, sequencing | | [120,121] |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Homo sapiens* | Tunisia | 319 | 2.2 | ELISA | | [122] |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Bos taurus, Capra hircus, Ovis aries* | Tunisia | 879 | 8.6 | ELISA, IFAT | | [123] |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Camelus dromedarius* | Tunisia | 273 | 89.7 | ELISA | | [124] |
| Crimean-Congo hemorrhagic fever | CCHF virus | Livestock | Egypt | 1022 | 3.1 | ELISA | | [125]. |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Camelus dromedarius* | Egypt | 34 | 8.8 | CFT | | [126] |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Ovis aries* | Egypt | 52 | 23 | CFT | | [126] |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Bos taurus* | Egypt | 161 | 1 | Agglutination test | | [127] |
| Crimean-Congo hemorrhagic fever | CCHF virus | *Camelus dromedarius* | Egypt | 4301 | 14 | IFAT, Agar gel-diffusion test | | [128] |
| Tick-borne encephalitis | TBE virus | *Ovis aries* | Tunisia | 263 | 38 | ELISA | | [129] |

*Abbreviations*: AHF, Alkhurma hemorrhagic fever; CFT, Complement fixation test; CCHF virus, Crimean-Congo hemorrhagic fever virus; ELISA, enzyme-linked immunosorbent assay; IFAT, immunofluorescence antibody test; ND, not defined; PCR, polymerase chain reaction; qPCR, quantitative polymerase chain reaction; RFLP, restriction fragment length polymorphism; RLB, reverse line blot hybridization; SOD, superoxide dismutase coding gene; TBE virus, tick-borne encephalitis virus.

Asterik (*) symbol indicates that the data provided represents the prevalence rate among small ruminant flocks
Serology¶ indicates that the serological test was not defined

distribution [192]. Cattle, goats, and sheep are the primary reservoirs of *C. burnetii* and the infected animals shed the bacterium in their birth products, milk, urine, and faeces [193]. Human infections occur via direct or indirect contact with aerosols or infected animal fluids. The disease in humans is usually asymptomatic; clinical manifestations include flu-like illness, but life-threatening complications, such as severe pneumonia, hepatitis, meningitis, and endocarditis have also been reported [193]. In 1955, the first human cases of Q fever were reported in North Africa [194]. Thus far, several studies have shown that the infection is endemic with significant difference in prevalence rates across North Africa.

In Algeria, *C. burnetii* was diagnosed as the cause of infective endocarditis in 1.9% (2/108) of cases [42]. A serological survey of 729 residents of Wilaya of Setif, an agro-pastoral region, identified *C. burnetii* antibodies in 15.5% of residents [41]. Residency in rural areas was the only risk factor associated with seropositivity [41]. Recently, *C. burnetii* was identified as the cause of febrile spontaneous abortion in three women out of 380 admitted cases [44]. Camels exhibited a high seroprevalence of *C. burnetii* at 71.2% (132/18) and 75.5% (139/18) [71,72]. The age of camels, herd size and tick infestation were significant risk factors [72]. A survey conducted in Setif province detected *C. burnetii* DNA in 6.98% (13/186) of cattle blood and 9% (18/200) of milk samples [67]. The DNA of *C. burnetii* was also isolated from the vaginal swabs of 21.3% (57/267) of small ruminants, using real-time PCR [78]. In addition, *C. burnetii* was identified in *Ixodes vespertilionis* collected from bats [147]; *H. erinaci* and *Rh. sanguineus* collected from *At. algirus* [63]; *Hy. excavatum, Hy. impeltatum, Hyalomma dromedarii,* and *Rhipicephalus bursa* ticks collected from camels, cattle, and sheep [63,71,148,149].

In Morocco, a *C. burnetii* seropositivity of 1% (1/300) was reported for blood donors from Casablanca and 18.3% (23/126) for citizens from

Fez [52]. Another investigation showed a *C. burnetii* seroprevalence rate of 57% (13/23) among small ruminant flocks [81]. In Tunisia, a serological survey of 500 blood donors living in Sousse and its rural surrounding areas identified *C. burnetii* antibodies in 26% of donors [53]. *Coxiella burnetii* was also serologically identified in 8.5% (6/47) and 2% (6/300) of acute febrile patients across two cohort studies conducted in Tunisian hospitals [54,58]. Another investigation of patients with chronic obstructive pulmonary disease detected *C. burnetii* in 6.6% of 240 cases [61]. The DNA of *C. burnetii* was identified in the vaginal swabs, placenta, or milk of 19.4% of small ruminants with a previous a history of abortion [82]. Furthermore, *C. burnetii* DNA has been isolated from *Hy. aegyptium, Ixodes* spp., *H. erinaci*, and *Rh. sanguineus* collected from *At. algirus* [153] and *Hy. impeltatum* and *Hy. dromedarii* collected from camels [40].

In Egypt, an earlier study detected antibodies for *C. burnetii* in 32% (285/883) of humans in the Delta region [49]. Another study in El-Minya Governorate reported a seropositivity of *C. burnetii* antibodies in 25.7% (9/35) of animal breeders [51]. Q fever was diagnosed in 5.6% (3/54) of acute hepatitis patients in Assiut [45]. Additionally, *C. burnetii* was identified as the underlying cause of 1.6% (1/63) and 1.5% (2/133) of cases of infective endocarditis in two different studies [46,47]. A nationwide survey of Q fever in 2,699 animals in Egypt detected a seropositivity rate of 40.7% (215/528), 19.3% (162/840), 11.2% (34/304), 8.9% (64/716), and 6.8% (21/311) in camels, cattle, buffalo, sheep, and goats, respectively [69]. Another investigation in Northern Egypt detected *C. burnetii* DNA in 33.6% (37/110) and 16.3% (13/80) of aborted sheep and goats, respectively [84]. Additionally, the bacterial DNA was isolated from *Hy. dromedarii, Hy. excavatum, Amblyomma variegatum, Hy. anatolicum, Rh. pulchellus, Ar. persicus,* and *Rh. sanguineus* collected from cattle, camel, buffalo, chickens, and rabbits [150–152].

**Table 2**
Summary of current knowledge on zoonotic tick-borne pathogens detected in ticks in North Africa.

| Pathogens | Possible tick vector(s) | Country | Vertebrate host(s)/vegetation | Detection method(s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|
| *Anaplasma phagocytophilum* | *Argas persicus* | Algeria | *Atelerix algirus*, domestic animals, *Gallus domesticus*, *Testudo graeca* | PCR, sequencing | *rpoB* | [130] |
| *Anaplasma phagocytophilum* | *Rhipicephalus sanguineus* | Egypt | *Canis familiaris* | PCR, sequencing | 16S rRNA | [131] |
| *Anaplasma phagocytophilum* | *Rhipicephalus sanguineus* | Egypt | *Canis familiaris* | PCR, sequencing | 16S rRNA | [132] |
| *Anaplasma phagocytophilum* | *Ixodes ricinus* | Tunisia | Vegetation | PCR, sequencing | 16S rRNA | [133] |
| *Anaplasma phagocytophilum* | *Hyalomma Aegyptium* | Tunisia | *Testudo graeca* | PCR, sequencing | 16S rRNA | [134] |
| *Anaplasma phagocytophilum* | *Hyalomma detrium* | Tunisia | *Bos taurus* | PCR, sequencing | 16S rRNA | [133] |
| *Anaplasma phagocytophilum* | *Hyalomma marginatum* | Tunisia | *Equus ferus* | Nested PCR | 16S rRNA | [24] |
| *Borrelia burgdorferi* | *Hyalomma anatolicum excavatum*, *Rhipicephalus sanguineus* | Egypt | *Bos taurus, Canis familiaris* | PCR, sequencing | *ospA* | [28] |
| *Borrelia burgdorferi* | *Rhipicephalus sanguineus* | Egypt | *Canis familiaris* | PCR, sequencing | 16S rRNA | [31] |
| *Borrelia burgdorferi* s.s. | *Ixodes ricinus* | Morocco, Tunisia | Vegetation | Culturing, PCR, sequencing, RFLP | 5S–23S rRNA spacer, *ospC, ospA* | [135] |
| *Borrelia burgdorferi* | *Ixodes ricinus* | Morocco | *Ovis aries*, vegetation | IFAT, PCR-RFLP | 5S–23S rRNA spacer | [136] |
| *Borrelia garinii* | *Ixodes ricinus* | Algeria | Vegetation | PCR, sequencing | 16S rRNA, *flaB* | [137] |
| *Borrelia garinii* | *Ixodes ricinus* | Morocco | *Ovis aries*, vegetation | IFAT, PCR-RFLP | 5S–23S rRNA spacer | [136] |
| *Borrelia garinii* | *Ixodes ricinus* | Morocco, Tunisia | Vegetation | Culturing, PCR, sequencing, RFLP | 5S–23S rRNA spacer, *ospC, ospA* | [135] |
| *Borrelia garinii* | *Ixodes ricinus* | Tunisia | Vegetation | PCR | 5S–23S rRNA spacer | [138] |
| *Borrelia lusitanae* | *Ixodes ricinus* | Tunisia | *Psammodromus algirus*, vegetation | IFAT, culturing, PCR-RFLP | 5S–23S rRNA spacer | [33] |
| *Borrelia lusitanae* | *Ixodes ricinus* | Tunisia | Vegetation | PCR | 5S–23S rRNA spacer | [138] |
| *Borrelia lusitanae* | *Ixodes ricinus* | Tunisia | Vegetation | PCR | 5S–23S rRNA spacer | [139] |
| *Borrelia lusitaniae* | *Ixodes ricinus* | Morocco, Tunisia | Vegetation | Culturing, PCR, sequencing, RFLP | 5S–23S rRNA spacer, *ospC, ospA* | [135] |
| *Borrelia lusitaniae* | *Ixodes ricinus* | Morocco | *Ovis aries*, vegetation | IFAT, PCR-RFLP | 5S–23S rRNA spacer | [136] |
| *Borrelia valaisiana* | *Ixodes ricinus* | Morocco, Tunisia | Vegetation | Culturing, PCR, sequencing, RFLP | 5S–23S rRNA spacer, *ospC, ospA* | [135] |
| *Borrelia crocidurae* | *Ornithodoros sonrai* | Algeria, Morocco, Tunisia | Burrows/nests, vegetation | PCR, sequencing | 16S–23S rRNA spacer, *flaB* | [140] |
| *Borrelia crocidurae* | *Ornithodoros erraticus* | Tunisia | Burrows/nests | PCR, sequencing | 16S rRNA, *flaB*, 16S–23S rRNA spacer, | [141] |
| *Borrelia crocidurae* | *Ornithodoros erraticus* s.l. | Morocco | Rodent burrows | PCR, nested PCR, sequencing | 16S–23S rRNA spacer, *flaB* | [39] |
| *Borrelia crocidurae,* | *Ornithodoros marocanus* | Morocco | Rodent burrows | PCR, sequencing | 16S–23S rRNA spacer | [142] |
| *Borrelia crocidurae* | *Ornithodoros sonrai* | Morocco | Houses, lands | PCR, sequencing | *flaB* | [143] |
| *Borrelia hispanica* | *Ornithodoros occidentalis* | Algeria | *Larus michahellis* nest, rodent burrows, sea bird nests | PCR, sequencing | *flaB* | [144] |
| *Borrelia hispanica* | *Ornithodoros erraticus* s.l. | Morocco | Rodent burrows | PCR, nested PCR, sequencing | 16S–23S rRNA spacer, *flaB* | [39] |
| *Borrelia hispanica* | *Ornithodoros occidentalis*, *Ornithodoros marocanus* | Morocco | Burrows/nests, vegetation | PCR, sequencing | 16S–23S rRNA spacer, *flaB* | [140] |
| *Borrelia hispanica* | *Ornithodoros marocanus* | Morocco | Rodent burrows | PCR, sequencing | 16S–23S rRNA spacer | [142] |
| *Borrelia hispanica* | *Ornithodoros marocanus* | Morocco | Rodent burrows | PCR, sequencing | 16S–23S rRNA spacer | [142] |
| *Borrelia hispanica* | *Ornithodoros marocanus* | Morocco | Rodent burrows | PCR, sequencing | 16S–23S rRNA spacer | [142] |
| *Borrelia merionesi* | *Ornithodoros erraticus* s.l. | Morocco | Rodent burrows | PCR, nested PCR, sequencing | 16S–23S rRNA spacer, *flaB* | [39] |
| *Borrelia merionesi.* | *Ornithodoros merioni, Ornithodoros coastalis* | Morocco | Burrows/nests, vegetation | PCR, sequencing | 16S–23S rRNA spacer, *flaB* | [140] |
| *Borrelia turicatae* | *Carios capensis* | Algeria | *Larus michahellis* nest, rodent burrows, sea bird nests | PCR, sequencing | *flaB* | [144] |
| *Borrelia turcica* | *Hyalomma aegyptium* | Algeria | *Testudo graeca nabeulensis* | qPCR, sequencing | *flaB* | [145] |
| *Ehrlichia ewingii* | *Heamaphysalis erinacei* | Tunisia | *Atelerix algirus* | PCR, nested PCR, qPCR, sequencing | 16S rRNA | [40] |
| *Ehrlichia ewingii* | *Hyalomma aegyptium* | Algeria | *Testudo graeca* | PCR, sequencing | 16S rRNA | [146] |
| *Coxiella burnetii* | *Hyalomma dromedarii, Hyalomma impeltatum, Hyalomma excavatum* | Algeria | *Camelus dromedarius* | qPCR, sequencing | *IS1111, htpB* | [71] |
| *Coxiella burnetii* | *Ixodes vespertilionis* | Algeria | *Chiroptera* spp. | qPCR | *IS30A* | [147] |
| *Coxiella burnetii* | *Hyalomma excavatum*, *Rhipicephalus bursa* | Algeria | *Bos taurus, Ovis aries* | qPCR, sequencing | *IS30, IS1111* | [148] |
| *Coxiella burnetii* | *Hyalomma impeltatum, Hyalomma dromedarii* | Algeria | *Camelus dromedarius* | qPCR, sequencing | *IS30, IS1111* | [149] |
| *Coxiella burnetii* | *Haemaphysalis erinaceii*, *Rhipicephalus sanguineus* s.l. | Algeria | *Atelerix algirus* | qPCR, sequencing | *IS30a, IS1111, gltA, sca1* | [63] |

**Table 2** (*continued*)

| Pathogens | Possible tick vector(s) | Country | Vertebrate host(s)/vegetation | Detection method (s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|
| *Coxiella burnetii* | *Hyalomma. dromedarii, Amblyomma variegatum, Hyalomma anatolicum anatolicum Rhipicephalus pulchellus* | Egypt | *Camelus dromedarius* | PCR, sequencing | *IS1111* | [150] |
| *Coxiella burnetii* | *Hyalomma dromedarii, Hyalomma excavatum* | Egypt | *Camelus dromedarius* | PCR, sequencing | *IS30A* | [151] |
| *Coxiella burnetii* | *Argas persicus, Hyalomma* spp., *Rhipicephalus sanguineus* | Egypt | *Bos taurus, Bubalus bubalis, Camelus dromedarius, Gallus domesticus, Oryctolagus domesticus* | PCR, qPCR, sequencing | *IS1111* | [152] |
| *Coxiella burnetii* | *Hyalomma impeltatum, Hyalomma dromedarii* | Tunisia | *Camelus dromedarius* | PCR, sequencing | *IS1111, htpB* | [153] |
| *Coxiella burnetii* | *Haemaphysalis erinacei, Ixodes* spp., *Hyalomma aegyptium, Rhipicephalus sanguineus* | Tunisia | *Atelerix algirus* | PCR, nested PCR, qPCR, sequencing | 16S rRNA | [40] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum rufipes, Hyalomma impeltatum, Hyalomma dromedarii* | Algeria | *Camelus dromedarius* | qPCR, sequencing | *gltA, ompA, sca2* | [154] |
| *Rickettsia aeschlimannii* | *Hyalomma excavatum, Hyalomma marginatum* | Algeria | *Bos taurus, Ovis aries* | PCR, sequencing | *ompA, ompB* | [148] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum, Hyalomma detrium detrium* | Algeria | *Bos taurus, Ovis aries* | PCR, sequencing | *gltA, ompA* | [155] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum, Hyalomma scupense, Hyalomma impeltatum.* | Algeria | *Bos taurus, Capra hircus, Ovis aries* | qPCR, sequencing | *gltA, ompA* | [156] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum, Hyalomma detritum, Rhipicephalus bursa* | Algeria | *Bos taurus* | qPCR, sequencing | *gltA*, 5S-23S rRNA spacer | [157] |
| *Rickettsia aeschlimannii* | *Hyalomma anatolicum excavatum, Hyalomma scupense* | Algeria | *Bos taurus* | PCR, qPCR, sequencing | *gltA, ompA* | [147] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum, Hyalomma detrium detrium* | Algeria | *Bos taurus* | PCR, sequencing | *gltA, ompA* | [155] |
| *Rickettsia aeschlimannii* | *Hyalomma aegyptium* | Algeria | *Testudo mauritanicum* | PCR, sequencing | *gltA, ompA* | [158] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum, Hyalomma detrium detrium* | Algeria | *Bos taurus* | PCR, sequencing | *gltA, ompA* | [155] |
| *Rickettsia aeschlimannii* | *Hyalomma aegyptium* | Algeria | *Testudo graeca nabeulensis* | qPCR, sequencing | *ompA* | [145] |
| *Rickettsia aeschlimannii* | *Hyalomma* spp. | Egypt | *Bos taurus, Bubalus bubalis, Camelus dromedarius* | PCR, qPCR, sequencing | *htrA* | [152] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum, Hyalomma impeltatum* | Egypt | *Bos taurus, Camelus dromedarius* | PCR, sequencing | *gltA, ompA, ompB, sca4, mppA-purC, dksA-xerC, rpmE-tRNAfMet* | [159] |
| *Rickettsia aeschlimannii* | *Hyalomma marginatum marginatum* | Morocco | Domestic animals | PCR, sequencing | *gltA, ompA* | [160] |
| *Rickettsia aeschlimannii* | *Hyalomma dromedarii* | Tunisia | *Camelus dromedarius* | qPCR, genotyping | *gltA, sca1* | [161] |
| *Rickettsia aeschlimannii* | *Hyalomma impeltatum, Hyalomma dromedarii* | Tunisia | *Camelus dromedarius* | Nested PCR, sequencing | *ompA, ompB* | [113] |
| *Rickettsia africae* | *Hyalomma aegyptium* | Algeria | *Testudo graeca nabeulensis* | qPCR, sequencing | *ompA* | [145] |
| *Rickettsia africae* | *Hyalomma marginatum Hyalomma dromedarii, Hyalomma impeltatum* | Egypt | *Bos taurus, Camelus dromedarius* | PCR, sequencing | *gltA, ompA, ompB, sca4, mppA-purC, dksA-xerC, rpmE-tRNAfMet* | [159] |
| *Rickettsia africae* | *Hyalomma marginatum* | Egypt | *Camelus dromedarius* | PCR, sequencing | *ompA, gltA, mppA, dksA, rpmE* | [162] |
| *Rickettsia africae* | *Hyalomma detritum, Hyalomma aegyptium* | Algeria | *Atelerix algirus*, domestic animals, tortoises | qPCR, sequencing | *gltA, ompA* | [130] |
| *Rickettsia africae* | *Hyalomma dromedarii* | Algeria | *Camelus dromedarius* | PCR, sequencing, multispacer typing | *gltA, ompA* | [163] |
| *Rickettsia africae* | *Hyalomma impeltatum, Hyalomma dromedarii* | Tunisia | *Camelus dromedarius* | Nested PCR, sequencing | *ompA, ompB* | [113] |
| *Rickettsia africaseptentrionalis* | *Ornithodoros erraticus, Ornithodoros normandi* | Algeria, Tunisia | Rodent burrows | PCR, sequencing | *gltA, ompB, cox1*, 16S rRNA | [164] |
| *Rickettsia barbariae* | *Rhipicephalus bursa* | Algeria | *Capra hircus, Ovis aries* | qPCR, sequencing | *gltA, ompA* | [156] |
| *Rickettsia barbariae* | *Hyalomma excavatum, Hyalomma marginatum* | Algeria | *Bos taurus, Ovis aries* | PCR, sequencing | *ompA, ompB* | [148] |
| *Rickettsia conorii conorii* | *Rhipicephalus sanguineus* | Algeria | *Atelerix algirus* | PCR, sequencing | *gltA, ompA* | [155] |
| *Rickettsia conorii* | *Rhipicephalus sanguineus* | Algeria | *Canis familiaris* | qPCR | *gltA, ompA* | [76] |
| *Rickettsia conorii conorii* | *Rhipicephalus sanguineus* | Morocco | Domestic animals | PCR, sequencing | *gltA, ompA* | [165] |
| *Rickettsia conorii* | *Rhipicephalus sanguineus* | Tunisia | *Canis familiaris, Capra hircus, Ovis aries* | RLB, PCR, sequencing | 5S-23SrRNA spacer, *ompA* | [166] |
| *Rickettsia conorii conorii* | *Rhipicephalus sanguineus* | Tunisia | *Canis familiaris, Capra hircus, Ovis aries* | PCR, sequencing | *gltA, ompA* | [103] |
| *Rickettsia conorii israelensis* | *Rhipicephalus sanguineus* | Tunisia | *Canis familiaris, Capra hircus, Ovis aries* | RLB, PCR, sequencing | 5S-23SrRNA spacer, *ompA* | [166] |
| *Rickettsia conorii israelensis* | *Rhipicephalus sanguineus* | Tunisia | *Canis familiaris, Capra hircus, Ovis aries* | PCR, sequencing | *gltA, ompA, ompB* | [103] |
| *Rickettsia helvetica* | *Ixodes ricinus, Rhipicephalus bursa* | Algeria | *Bos taurus* | qPCR | | [167] |
| *Rickettsia helvetica* | *Ixodes ricinus* | Algeria | *Bos taurus* | qPCR, sequencing | *gltA*, 5S-23SrRNA spacer | [157] |
| *Rickettsia helvetica* | *Ixodes ricinus* | Algeria | *Bos taurus*, vegetation | qPCR, sequencing | *gltA, ompA* | [168] |
| *Rickettsia helvetica* | *Ixodes ricinus* | Morocco | Vegetation | PCR, sequencing | *gltA, ompA* | [160] |

**Table 2** (*continued*)

| Pathogens | Possible tick vector(s) | Country | Vertebrate host(s)/vegetation | Detection method (s) | Target gene(s) | Reference |
|---|---|---|---|---|---|---|
| *Rickettsia helvetica* | *Hyalomma impeltatum, Hyalomma dromedarii* | Tunisia | *Camelus dromedarius* | Nested PCR, sequencing | *ompA, ompB* | [113] |
| *Rickettsia helvetica* | *Ixodes ricinus* | Tunisia | Vegetation | PCR, sequencing | *gltA, ompA* | [169] |
| *Rickettsia helvetica* | *Ixodes ricinus* | Tunisia | Vegetation | PCR, sequencing | *gltA, ompA* | [169] |
| *Rickettsia lusitaniae* | *Rhipicephalus sanguineus* | Tunisia | *Atelerix algirus* | PCR, nested PCR, qPCR, sequencing | *ompB, gltA* | [40] |
| *Rickettsia massiliae* | *Ixodes ricinus, Rhipicephalus bursa* | Algeria | *Bos taurus* | qPCR | ND | [167] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus, Rhipicephalus turanicus* | Algeria | *Atelerix algirus, Bos taurus, Capra hircus* | PCR, sequencing | *gltA, ompA* | [155] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus, Hyalomma* spp. | Algeria | *Bos taurus* | qPCR, sequencing | *gltA*, 5S-23S rRNA spacer | [157] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* s.l., *Rhipicephalus bursa* | Algeria | *Capra hircus, Ovis aries* | qPCR, sequencing | *gltA, ompA* | [156] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* | Algeria | *Canis familiaris* | qPCR | *gltA, ompA* | [76] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* | Algeria | *Atelerix algirus, Paraechinus aethiopicus* | qPCR, sequencing | *gltA, ompA* | [170] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* s.l. | Algeria | *Bos taurus, Canis familiaris, Canis lupaster, Ovis aries, Sus scrofa* | PCR, qPCR, sequencing | *gltA, ompA* | [147] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* s.l. | Algeria | *Atelerix algirus* | qPCR | *gltA, sca1* | [63] |
| *Rickettsia massiliae* | *Rhipicephalus turanicus* | Algeria | *Atelerix algirus, Bos taurus, Capra hircus* | PCR, sequencing | *gltA, ompA* | [155] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* | Morocco | Domestic animals | PCR, sequencing | *gltA, ompA* | [160] |
| *Rickettsia massiliae* | *Rhipicephalus bursa* | Morocco | Domestic animals | PCR, sequencing | *gltA, ompA* | [165] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* | Tunisia | *Canis familiaris, Capra hircus, Ovis aries* | RLB, PCR, sequencing | *ompA* | [166] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* | Tunisia | *Atelerix algirus* | PCR, nested PCR, qPCR, sequencing | *ompB, gltA* | [40] |
| *Rickettsia massiliae* | *Rhipicephalus turanicus* | Tunisia | *Ovis aries, Capra hircus* | PCR, sequencing | *gltA, ompA, ompB* | [171] |
| *Rickettsia massiliae* | *Rhipicephalus sanguineus* | Tunisia | *Canis familiaris, Capra hircus, Ovis aries* | PCR, sequencing | *gltA, ompA* | [103] |
| *Rickettsia mauretanica* | *Ornithodoros occidentalis* | Morocco | Rodent/burrows | PCR, sequencing | *gltA, ompB, cox1*, 16S rRNA | [164] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Algeria | *Bos taurus* | qPCR, sequencing | *gltA*, 5S-23S rRNA spacer | [157] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Algeria | Vegetation | qPCR, sequencing | *gltA, ompA* | [137] |
| *Rickettsia monacensis* | *Ixodes ricinus, Rhipicephalus bursa* | Algeria | *Bos taurus* | qPCR | | [167] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Algeria | *Atelerix algirus*, domestic animals | qPCR, sequencing | *gltA, ompA* | [130] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Algeria | *Bos taurus* | PCR, sequencing | *gltA, ompA* | [172] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Morocco | Vegetation | PCR, sequencing | *gltA, ompA* | [160] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Morocco | Vegetation | qPCR, sequencing | *gltA, ompA* | [165] |
| *Rickettsia monacensis* | *Rhipicephalus sanguineus* | Tunisia | *Capra hircus, Ovis aries* | PCR, sequencing | *gltA, ompA, ompB* | [171] |
| *Rickettsia monacensis* | *Ixodes ricinus* | Tunisia | Vegetation | PCR, sequencing | *gltA, ompA* | [169] |
| *Rickettsia monacensis* | *Hyalomma impeltatum, Hyalomma dromedarii* | Tunisia | *Camelus dromedarius* | Nested PCR, sequencing | *ompA, ompB* | [113] |
| *Rickettsia raoultii* | *Ixodes ricinus, Rhipicephalus bursa* | Algeria | *Bos taurus* | qPCR | ND | [167] |
| *Rickettsia raoultii* | *Dermacentor marginatus* | Morocco | Domestic animals | PCR, sequencing | *gltA, ompA* | [160] |
| *Rickettsia sibirica mongolitimonae* | *Hyalomma aegyptium* | Algeria | *Testudo graeca nabeulensis* | qPCR, sequencing | *ompA* | [145] |
| *Rickettsia slovaca* | *Haemaphysalis punctata, Dermacentor marginatus* | Algeria | *Sus scrofa algira* | PCR, qPCR, sequencing | *gltA, ompA* | [147] |
| *Rickettsia slovaca* | *Dermacentor marginatus* | Algeria | *Bos taurus*, vegetation | qPCR, sequencing | *gltA, ompA* | [168] |
| *Rickettsia slovaca* | *Dermacentor marginatus* | Morocco | Domestic animals | PCR, sequencing | *gltA, ompA* | [160] |
| *Babesia motasi* | *Rhipicephalus turanicus, Rhipicephalus annulatus* | Tunisia | *Capra hircus, Ovis aries* | PCR, RLB | 18S rRNA | [173] |
| *Babesia motasi* | *Rhipicephalus annulatus* | Tunisia | *Bos taurus* | PCR, RLB | 18S rRNA | [174] |
| Crimean-Congo hemorrhagic fever virus | *Hyalomma aegyptium* | Algeria | *Testudo graeca* | PCR, sequencing | nucleoprotein | [175] |
| Crimean-Congo hemorrhagic fever virus | *Hyalomma dromedarii, Hyalomma rufipes* | Egypt | *Camelus dromedarius* | Nested PCR, sequencing | nucleoprotein | [176] |
| Crimean-Congo hemorrhagic fever virus | *Hyalomma dromedarii, Hyalomma excavatum* | Egypt | *Camelus dromedarius* | PCR, sequencing | nucleoprotein | [177] |
| Crimean-Congo hemorrhagic fever virus | *Hyalomma impeltatum* | Tunisia | *Camelus dromedarius* | qPCR | nucleoprotein | [124] |
| Crimean-Congo hemorrhagic fever virus | *Hyalomma marginatum* | Morocco | Migratory birds | Nested PCR, sequencing | nucleoprotein | [178] |
| Tick-borne encephalitis virus | *Ixodes ricinius* | Tunisia | *Bos taurus*, vegetation | Heminested reverse transcription PCR | ND | [179] |

*Abbreviations*: IFAT, immunofluorescence antibody test; ND, not defined; PCR, polymerase chain reaction; qPCR, quantitative polymerase chain reaction; RFLP, restriction fragment length polymorphism; RLB, reverse line blot hybridization

#### 2.1.5. Tick-borne rickettsioses

Tick-borne rickettsioses are systemic febrile bacterial zoonoses caused by spotted fever group *Rickettsia* and share a distinctive clinical presentation including eruptive fever, maculopapular rash, and occasionally eschar formation at the tick bite site [195]. In North African countries, at least ten zoonotic tick-transmitted rickettsiae, have been isolated from ticks or human cases, including *Rickettsia conorii conorii*, *Rickettsia conorii israelensis*, *Rickettsia aeschlimannii*, *Rickettsia sibirica mongolitimonae*, *Rickettsia massiliae*, *Rickettsia slovaca*, *Rickettsia raoultii*, *Rickettsia monacensis*, *Rickettsia africae,* and *Rickettsia helvetica.*

##### 2.1.5.1. Mediterranean spotted fever (MSF). Mediterranean spotted fever (MSF) is caused by *R. conorii conorii.* MSF is the most common tick borne-rickettsiosis in North-Africa [196]. In Algeria, the documented cases have been steadily increasing. In a prospective study performed in Oran, 53 cases of MSF were diagnosed using serologic methods [91]. Severe forms of MSF, characterised by neurologic manifestations and multiple organ involvement, occurred in 42% of cases and three patients died [91]. In another study including 36 children from Oran, 24 were diagnosed with MSF using serology [89]. In total 62.5% of the sero-positive cases were hospitalised with moderate fever, eschars, spleno-megaly, digestive disorders (vomiting and diarrhoea) and seizures were reported in two children [89]. Simultaneously, 167 patients with MSF were diagnosed at Oran hospital using serological and molecular methods. Of those, 49% were hospitalised with severe manifestations including neurologic symptoms and multiple organ involvement [92]. Recently, in a prospective study from North-central Algeria, Tizi-Ouzou, 57 (3.3%/166) cases with fever and rash were confirmed as MSF using serological and molecular methods [95]. In Morocco, 21 MSF patients in Casablanca were diagnosed; 14% had multiple inoculation eschars and the case fatality rate was 5% among these patients [100]. In addition, MSF was reported in a 14-month-old boy who had neurological symptoms. The clinical examination showed maculopapular eruptions, and a necrotic eschar at the right ear. Diagnosis was confirmed using immunofluorescence [99]. In Tunisia, a prospective study including 30 MSF patients at Monastir detected unilateral or bilateral posterior segment involvement in 83% of patients. Most of these ocular complications were resolved after a few weeks with restoration of visual acuity [105]. In Sousse (central Tunisia), high prevalence of MSF (52.1%/119) was confirmed among febrile patients using serological and molecular methods [107]. *Rickettsia conorii* infection was also diagnosed in a 4-years old Libyan girl, presented with fever and generalised maculopapular rash, using immunofluorescence [98]. In Egypt, circulation of antibodies reactive to *R. conorii* was reported among humans and rodents [49,97,109]. Furthermore, *R. conorii conorii* DNA was isolated from *Rh. sanguineus* ticks from Tunisia [103,166], Algeria [76,155], and Morocco [165], using molecular tools.

##### 2.1.5.2. Israeli spotted fever (ISF). Israeli spotted fever (ISF) is caused by *R. conorii israelensis.* ISF has a clinical presentation similar to that of other spotted fever group rickettsial infections; however, the inoculation eschar and history of tick exposure are unlikely to be noticed. In Tunisia, three cases of ISF from Sfax were admitted with a history of fever and cutaneous maculopapular rash. Diagnosis was confirmed based on the molecular detection of rickettsial DNA in skin biopsies [103,110]. Additionally, *R. conorii israelensis* was detected in *Rh. sanguineus* ticks from Tunisia [103,166].

##### 2.1.5.3. Rickettsia aeschlimannii infection. The first documented human infection with *R. aeschlimannii* was in a French traveller who returned from a trip to Morocco [112]. Later a *R. aeschlimannii* infection was reported in two Algerian patients [111]. Additionally, a Tunisian patient was diagnosed with *R. aeschlimannii* and the bacterium was isolated from *Rattus rattus* and *Meriones shawi* [101,114]. *Rickettsia aeschlimannii* was also identified by molecular tools in *Rh. bursa* and several *Hyalomma*

ticks, including *Hy. aegyptium* collected from tortoises in Algeria [145,158], *Hy. impeltatum*, *Hy. dromedarii*, *Hyalomma scupense*, *Hy. rufipes*, *Hy. detrium detrium*, *Hy. anatolicum,* and *Hy. excavatum* ticks collected from camels, cattle, buffalo, and sheep in Algeria, Morocco, Tunisia, and Egypt [113,147,148,152,154–157,159–161].

##### 2.1.5.4. Rickettsia sibirica mongolitimonae infection. *Rickettsia sibirica mongolitimonae* has been reported from two cases in North Africa. The first was a 62-year-old French female who had returned from a trip to southern Algeria [197]. She had been in contact with camel ticks. The second was a 52-year-old French man who returned from a trip to southern Egypt. He was presented with fever, an inoculation eschar and axillary lymphadenopathy [115]. In addition, *R. sibirica mongolitimonae* has been identified in *Hy. aegyptium* collected from Nabeul tortoises in Algeria [145].

##### 2.1.5.5. Rickettsia massiliae infection. In a study of 101 Tunisian patients presenting with fever and cutaneous rashes and/or eschars, *R. massiliae* has been identified in a skin biopsy of one patient [102]. *Rickettsia massiliae* has also been detected in Tunisian camels (0.34%/293) [113], and rodents (*Ra. rattus* and *M. shawi*) [114]. Additionally, *R. massiliae* was isolated from *I. ricinus,* and *Rh. bursa, Rh. turanicus,* and *Rh. sanguineus* ticks in Algeria [63,76,147,155–157,167,170]. It has also been identified in *Rh. sanguineus* and *Rh. bursa* ticks in Morocco [160,165] and Tunisia [40,103,166,171].

##### 2.1.5.6. Other tick-borne rickettsial infections. *Rickettsia slovaca* and *R. raoultii,* are associated with eschars and lymphadenopathy following tick bites. *Rickettsia slovaca* was isolated from *Sus scrofa algira* in Algeria (5.4%/92) using molecular methods [116]. *Rickettsia slovaca* was also detected in *Dermacentor marginatus* ticks in Morocco [160] and in *Hy. aegyptium*, *Haemaphysalis punctata*, and *D. marginatus* in Algeria [145,147,168]. Additionally, *R. raoultii* was isolated from *D. marginatus* in Morocco [160], *Rh. bursa,* and *I. ricinus* in Algeria [167].

*Rickettsia monacensis* was detected in Tunisian camels (1.37%/293) [113] and *I. ricinus* in Morocco [160,165], *I. ricinus* and *Rh. bursa* ticks in Algeria [130,137,157,167,172], and *Hy. impeltatum, Hy. dromedarii, I. ricinus,* and *Rh. sanguinius* in Tunisia [113,169,171].

*Rickettsia africae,* the agent of African tick-bite fever, has been detected in *Ra. rattus* and *M. shawi* in Tunisia [114]. *Rickettsia africae* has also been identified in *Hy. aegyptium* collected from Algerian *Testudo graeca nabeulensis* and *Hyalomma* ticks including, *Hy. marginatum H. dromedarii, H. impeltatum Hy. detritum,* and *Hy. aegyptium* collected from camels and cattle in Algeria, Tunisia, and Egypt [113,130,145,159,162,163].

*Rickettsia helvetica* was detected in camels (0.34%/293) [113], and rodents (*Ra. rattus* and *M. shawi*) in Tunisia [114]. Furthermore, *R. helvetica* was isolated from *I. ricinus, Rh. bursa, Hy. dromedarii,* and *Hy. impeltatum* in Algeria, Tunisia, and Morocco [113,157,160,167–169].

*Rickettsia mauretanica* was identified in *Ornithodoros occidentalis* from Morocco; *Rickettsia africaseptentrionalis* has been detected in *Ornithodoros erraticus* from Algeria [164]; *Rickettsia barbariae* was isolated from *Rh. bursa* ticks in Algeria [156]; *Rickettsia lusitaniae* was isolated from *Rh. sanguineus* ticks collected from *At. algirus* in Tunisia [40].

### 2.2. Parasitic diseases

#### 2.2.1. Babesiosis

Human babesiosis is a parasitic zoonosis caused by infection with *Babesia* spp. including, but not limited to *Babesia motasi, B. microti, B. divergens, B. duncani,* and *B. venatorum* [198]. This disease is primarily transmitted by ixodid ticks. Infection is usually asymptomatic and self-limiting in healthy individuals, and occasionally presented with non-specific flu-like symptoms such as fever, malaise, chills and shortness of breath [199]. However, severe complications including haemolytic

anaemia, splenomegaly, hepatomegaly, renal failure, myocardial infarction, and death can occur in immunocompromised individuals [200,201].

In Egypt, human babesiosis was serologically detected in three cases who recovered following treatment [202–204]. Additionally, a serosurvey of 43 blood donors detected *Babesia* antibodies in five Egyptians [205]. In Tunisia, *B. divergens* was isolated from a cow in North-western Tunisia and later, 137 cattle selected from 35 farms tested positive for *B. divergens* infection using indirect immunofluorescence [118,119]. Additionally, *B. motasi* was molecularly detected in *Rhipicephalus annulatus* and *Rh. turanicus* ticks [173,174].

### 2.3. Viral diseases

#### 2.3.1. Alkhumra hemorrhagic fever (AHF)

Alkhumra hemorrhagic fever (AHF) is an emerging haemorrhagic disease in humans, caused by the flavivirus: AHF virus (AHFV). This disease is transmitted to humans through direct contact with infected animals or via tick bites [206,207]. AHFV was primarily isolated from butchers and residents of Jeddah, Saudi Arabia in 1995 [208]. AHFV RNA was also detected in *Ornithodoros savignyi,* and *Hy. dromedarii* ticks [206,209]. Since then, new sporadic infections have been documented in Saudi Arabia, and subsequent cases of AHF have been reported in India, Djibouti, and Europe [210]. In Egypt, AHFV was isolated from three Italian tourists who had visited a camel market at Shalateen, Southern Egypt. During their visit, one of these tourists experienced a tick bite. Several days after returning to Italy, they were hospitalized due to high fever, chills, malaise, nausea, vomiting, and blurred vision [120,121].

#### 2.3.2. Crimean-Congo hemorrhagic fever (CCHF)

Crimean-Congo hemorrhagic fever (CCHF) is a serious tick-borne disease present in many countries throughout Africa, Asia, and Europe [211]. CCHF is caused by the CCHF virus (CCHFV) which belongs to the *Orthonairovirus* genus (family Nairoviridae). CCHFV is maintained in enzootic cycles between ticks, birds, and mammals, while humans are dead-end hosts [212]. Human infections occur through tick bites or by direct contact with blood or tissues from diseased animals or patients [213]. Although animals do not show symptoms, human CCHF infections progress through four phases: incubation, prehemorrhagic, hemorrhagic, and convalescence [214]. The incubation period varies depending on the mode of infection; for infections originating from tick bites, it can last up to 9 days, whereas for exposure from infected blood or tissues, it can last up to 13 days. The prehemorrhagic phase is characterised by sudden onset of fever, headache, joint pain, diarrhea, nausea, and abdominal pain. The hemorrhagic phase results in petechiae, hematomas, gastrointestinal bleeding, and the case fatality rate ranges between 5–50% [214]. In the Mediterranean basin, *Hyalomma* spp. are the main vectors of the CCHFV, and domestic animals (such as camels, cattle, and sheep) and wild species (such as birds, hedgehogs, and hares) are important hosts of the CCHFV [212].

In Tunisia, the seroprevalence of the CCHFV among acute febrile patients and abattoir workers was 2.7% and 5.2% in Sousse, Sfax, and Mahdia, respectively [122]. However, the CCHFV RNA was not detected in ticks collected from Northern and Southern Tunisia [122]. Antibodies against CCHFV have been detected in camels (89.7%) in Southern Tunisia and viral RNA was detected in *Hy. impeltatum* ticks but not in the camel sera [124]. Recently, CCHFV antibodies have also been reported in ruminants (cattle, sheep, and goats) in Tunisia [123]. In Algeria, the CCHFV was isolated from *Hy. aegyptium* ticks collected from tortoises in Laghouat Province [175]. In Morocco, the CCHFV was detected in ticks collected from migratory birds [178]. In Egypt, serological evidence of viral circulation among livestock has been reported [126–128]. In a serosurvey conducted from September 2004 to August 2005, 3.13% of sera from 1,022 animals (cattle, buffalo, sheep, and goats) tested positive for the CCHFV [125]. Additionally, the CCHFV RNA was detected

from *Hy. excavatum, Hy. rufipes*, and *Hy. dromedarii* ticks [176,177].

#### 2.3.3. Tick-borne encephalitis

Tick-borne encephalitis (TBE) is a potentially life-threatening neuroviral infection that occurs in Europe and Asia. This disease is caused by the TBE virus (TBEV), a flavivirus which is usually transmitted via tick bites or occasionally through consumption of raw milk taken from infected sheep, goats, or cows [215]. The main vectors of the TBV in Europe are ixodid ticks, mainly *I. ricinus* and *I. persulcatus*. The TBEV causes febrile illness which may include severe neurological symptoms. Although several licensed vaccines are available, the incidence of TBE is increasing in Europe [216].

Arboviral infections including TBE have been overlooked and underestimated in North Africa. Following the detection of the first fatal case of TBE in southern Italy is important [217], especially given the countries close proximity to Northern Africa and its role as a significant pathway for migratory birds harboring *I. ricinus* [218], the TBEV was serologically diagnosed in Tunisian sheep and importantly was isolated from *I. ricinus* ticks from Northwestern Tunisia [129,179]. These findings support the presence of TBEV in Tunisia and possibly other North African countries.

## 3. Human-biting ticks of North Africa

Although many tick species occur in North Africa, not all of these infest humans, and as such, some do not pose a direct threat to public health. The authors recognise a total of 54 human-biting tick species in North Africa, of which 42 are hard ticks (Ixodidae) and 12 are soft ticks (Argasidae) (Table 3). Although the primary interest in ticks stems from their role as vectors of zoonotic pathogens, ticks alone are capable of directly causing a range of important diseases. Perhaps the most common disease associated with ticks in acariasis which can range from mild infestations causing only itchiness and swelling around the location of the tick bite, through to more extreme conditions such as otoacariasis which can result in extreme pain, dizziness, and nausea [219]. In fact, the common North African tick *Hy. marginatum* is reported to commonly cause otoacariasis [220].

Ticks are also notorious for the paralysis and toxicosis sometimes associated with their bites [221]. Toxicosis is considered to be a pathological condition caused by the action of a toxin, while paralysis (with respect to tick bites) is the partial or complete loss of movement or muscle function due to the presence of a toxin (typically from the saliva of a tick). Therefore, we regard tick paralysis to be a specialised form of tick-bite induced toxicosis. A number of North African tick species have been reported to cause paralysis in humans including *Ixodes hexagonus*, *Ixodes redikorzevi*, *Rh. annulatus*, *Rhipicephalus praetextatus*, *Rhipicephalus simus*, and *Dermacentor variabilis* [222]. Simply because a tick can induce paralysis in one host species does not necessarily mean that it can induce paralysis in another host species. For example, while *Rhipicephalus evertsi* (another common North African tick) frequently causes paralysis in domestic sheep (*Ovis aries*), it is not known to cause paralysis in rodents or humans [223]. Although they are not reported to cause paralysis in humans, a number of other North African ticks are known to cause toxicosis including *O. savignyi* which causes sand tampan toxicosis which is more common in livestock, though can also impact humans [224].

A newly recognised, though widespread, threat to public health is tick-induced mammalian meat allergy (TIMMA) [225]. TIMMA is caused when individuals are sensitised to galactose-alpha-1,3-galactose (alpha-gal) by a tick bite. Subsequent exposure to alpha-gal can result in an allergic response. As alpha-gal is ubiquitous in mammalian meat, the patient often suffers repeated allergic reactions when ingesting mammalian meat, or food/drink products containing alpha-gal [226]. Members of a number of different tick genera have been shown to induce TIMMA including *Ixodes*, *Amblyomma*, and *Haemaphysalis* [225]. Among the species implicated in TIMMA, *Am. variegatum* is the only member of

**Table 3**
Human-biting tick species of North Africa.

| Family | Species | Egypt | Libya | Tunisia | Algeria | Morocco | Spanish exclave(s) | Distribution reference(s) | Human infestation frequency | Infestation reference |
|---|---|---|---|---|---|---|---|---|---|---|
| Argasidae | Argas persicus | + | + | | + | + | | [229,230] | Low | [231] |
| Argasidae | Argas reflexus | + | + | + | | | | [229] | Low | [232] |
| Argasidae | Argas transgariepinus | + | | | + | + | | [229] | Low | [233] |
| Argasidae | Argas vespertilionis | + | + | | + | + | | [229] | Low | [231] |
| Argasidae | Ornithodoros capensis | | | | + | | | [230] | Low | [234] |
| Argasidae | Ornithodoros coniceps | + | | + | | + | | [229] | Low | [235] |
| Argasidae | Ornithodoros erraticus | + | + | + | + | + | | [229] | Low | [236] |
| Argasidae | Ornithodoros foleyi | | + | | | | | [237] | Low | [238] |
| Argasidae | Ornithodoros maritimus | | | + | | + | | [229] | Low | [236] |
| Argasidae | Ornithodoros salahi | + | | | | | | [239] | Low | [239] |
| Argasidae | Ornithodoros savignyi | + | + | | + | | | [230,238,240] | Medium | [236] |
| Argasidae | Ornithodoros tholozani | + | + | | | | | [229] | Medium | [229] |
| Ixodidae | Amblyomma gemma | + | | | | | | [241] | Low | [242] |
| Ixodidae | Amblyomma hebraeum | + | | | | | | [243] | High | [242] |
| Ixodidae | Amblyomma lepidum | + | | | | | | [241] | Low | [242] |
| Ixodidae | Amblyomma marmoreum | + | | | | | | [244] | Medium | [242] |
| Ixodidae | Amblyomma variegatum | + | | | | | | [241] | High | [242] |
| Ixodidae | Dermacentor marginatus | | | + | + | + | | [229] | High | [242] |
| Ixodidae | Haemaphysalis erinacei | + | | + | + | | | [229,245] | Low | [242] |
| Ixodidae | Haemaphysalis parva | + | | | | | | [246] | High | [242] |
| Ixodidae | Haemaphysalis punctata | | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Haemaphysalis sulcata | | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Hyalomma aegyptium | + | | + | + | + | + | [229,247] | High | [242] |
| Ixodidae | Hyalomma albiparmatum | + | | | | | | [248] | Low | [242] |
| Ixodidae | Hyalomma anatolicum | + | + | | + | | | [229] | High | [242] |
| Ixodidae | Hyalomma dromedarii | + | + | + | + | | | [229] | Low | [242] |
| Ixodidae | Hyalomma excavatum | + | + | + | + | | | [229] | High | [242] |
| Ixodidae | Hyalomma impeltatum | + | + | + | + | + | | [229] | Low | [242] |
| Ixodidae | Hyalomma lusitanicum | + | + | + | + | + | | [229,249] | Medium | [242] |
| Ixodidae | Hyalomma marginatum | + | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Hyalomma rufipes | + | + | + | + | | | [229,241] | Low | [242] |
| Ixodidae | Hyalomma schulzei | + | | | | | | [250] | Low | [242] |
| Ixodidae | Hyalomma scupense | + | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Hyalomma truncatum | + | | | + | | | [230,241] | Medium | [242] |
| Ixodidae | Hyalomma turanicum | + | | | | | | [251] | High | [242] |
| Ixodidae | Ixodes frontalis | + | | | | + | | [229] | Low | [242] |
| Ixodidae | Ixodes hexagonus | | | | + | | | [230] | High | [242] |
| Ixodidae | Ixodes redikorzevi | + | | | | | | [252] | Medium | [242] |
| Ixodidae | Ixodes ricinus | + | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Ixodes vespertilionis | | | | + | | | [230] | Low | [242] |
| Ixodidae | Rhipicephalus annulatus | + | + | + | + | + | | [229] | Medium | [242] |
| Ixodidae | Rhipicephalus appendiculatus | + | | | | | | [249] | Medium | [242] |
| Ixodidae | Rhipicephalus bursa | + | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Rhipicephalus decoloratus | + | | | | | | [252] | Low | [242] |
| Ixodidae | Rhipicephalus evertsi | + | | | + | | | [230,252] | Medium | [242] |
| Ixodidae | Rhipicephalus guilhoni | + | | | + | | | [230,253] | Low | [242] |
| Ixodidae | Rhipicephalus humeralis | + | | | | | | [248] | Low | [242] |
| Ixodidae | Rhipicephalus muhsamae | + | | | | | | [254] | Low | [242] |
| Ixodidae | Rhipicephalus praetextatus | + | | | | | | [255] | Low | [242] |
| Ixodidae | Rhipicephalus pulchellus | + | | | | | | [248] | Medium | [242] |
| Ixodidae | Rhipicephalus rossicus | + | | | | | | [229] | Low | [242] |
| Ixodidae | Rhipicephalus sanguineus | + | + | + | + | + | | [229] | High | [242] |
| Ixodidae | Rhipicephalus simus | + | | | | | | [252] | Medium | [242] |
| Ixodidae | Rhipicephalus turanicus | + | + | + | + | + | | [229,256] | High | [242] |

the group which occurs in North Africa [225]. Although TIMMA has not yet been reported from North Africa, this is likely a case of lack of awareness among doctors, rather than absence of TIMMA. Given that at least one tick species known to cause TIMMA occurs in North Africa, it is likely that cases will increasingly be recognised in future. Tick-bite anaphylaxis is another, often life-threatening, allergic disease associated with ticks. It is often caused by the body responding to tick salivary antigens with the over-release of immunoglobulin E (IgE) resulting in anaphylaxis. If not treated quickly, tick-bite anaphylaxis can prove fatal, thus making it a particularly serious disease [227]. At least two North

African ticks, *Rh. bursa* or *Hy. marginatum* have been reported to cause tick-bite anaphylaxis [228].

## 4. The environmental aspects of ticks and tick-borne pathogens in North Africa

Ticks and tick-borne pathogens also have the potential to impact the environment. As the climate changes, the distribution and abundance of many tick species may shift, and this may allow them to invade new ecosystems and interact with naïve wildlife populations. For example, a study estimating the future spatial distribution of *I. ricinus* under climate change scenarios showed overlap between the North African region and Europe [257]. Other environmental factors, such as habitat fragmentation and modifications, may also play a role in complicating disease cycles associated with ticks and wildlife [258]. To understand how future climate and land use scenarios may impact the distribution and ecology of North African ticks and tick-borne diseases in Europe and North Africa, extensive research is needed. Although modeling is a useful approach for predicting the future distribution of ticks in a changing world, a prolonged field work is also required to elucidate the complex nature of ticks-wildlife-pathogen relationships.

## 5. Trans-Mediterranean movement of ticks and tick-borne pathogens: Challenges and opportunities

### 5.1. Drivers of trans-Mediterranean tick movement

Numerous bird species travel across the Mediterranean Sea annually from their breeding sites in Europe to their wintering sites in Africa, and then back again. Ticks infesting these birds are frequently transported with them across the Mediterranean between Europe and North Africa in a bidirectional flow. This cross-Mediterranean movement of ticks (and tick-borne pathogens) creates a dual health threats for both Europe and North Africa as it provides the opportunity for some of these species to invade and establish populations in new regions [259,260].

The CCHFV was reported from *Hy. lusitanicum* ticks in Spain, and was suggested to have been introduced via migratory birds moving over the Mediterranean from North Africa [261]. The CCHFV was detected in spring and autumn bird migrants in Turkey [262]. AHFV RNA was isolated from larvae and nymphs of *Hy. rufipes* ticks collected from northbound migratory birds caught in Greece and Turkey [263]. In another investigation of northward migrating birds in Italy, *Hy. rufipes*, *Hy. marginatum*, and *Am. variegatum* were the most abundant species infesting birds and the pathogens *R. aeschlimannii* and *R. africae* were also detected [264]. In North Africa, a solitary investigation detected CCHFV in *Hy. marginatum* ticks removed from migratory birds in Morocco [178]. Shifts in climate, trending towards warmer temperatures, will also likely make significant regions of southern Europe more favourable for North African ticks (Buczek et al. 2020). Therefore, the effects of climate change on migratory birds and North African ticks will likely become a growing problem in Europe over the coming decades.

Another potential driver of the trans-Mediterranean movement of ticks and tick-borne pathogens is the importation of animals from North Africa to Europe. A surveillance of exotic tick species on dogs travelling to the UK, detected *Rh. sanguineus* (the primary vector of *R. conorii conorii*) originating from Tunisia [265]. In another study, *Hy. aegyptium* was introduced into Italy and Spain through illegal importation of tortoises (*T. graeca)* from Algeria [266,267]. Importantly, further investigation of those *T. graeca,* illegally imported to Italy, led to the detection of *E. ewingii,* the causative agent of human ehrlichiosis [146]. Clearly, enhanced surveillance is necessary to detect and control North African ticks originating from the exotic pet trade to prevent the inadvertent establishment of exotic North African tick species in Europe.

Though far less significant than migratory birds or exotic animals, travellers across the Mediterranean also have the capacity to transport non-native ticks to new regions. For example, McGarry [268] reported the importation of *Hy. rufipes* into Europe on a traveller returning from Egypt. The movement of large numbers of illegal migrants across the Mediterranean also has the potential to act as a bridge for non-native ticks and tick-borne diseases to enter southern Europe from North Africa.

### 5.2. Addressing the One Health challenge of trans-Mediterranean tick movement

The trans-Mediterranean movement of ticks between Europe and North Africa presents a serious challenge to not only human health, but also that of animals and ecosystems. As such, a trans-national One Health approach is necessary to bring together researchers and policy makers from both European and North African countries. The advanced economies of Europe have both funds and a strong research capacity, exemplified in the European Centre for Disease Prevention and Control. Although the developing economies of North Africa lack ample funds and a strong research capacity, they possess the significant technical experience required to undertake widescale surveillance programs across the vast territories of North Africa. Clearly, collaboration between the two could combine the fieldwork, funds, and research capacity required to generate a significantly higher resolution understanding of the diversity, distribution, and ecology of ticks and zoonotic tick-borne pathogens in North Africa. This understanding could then support efforts in Europe to predict and prevent the flow of these harmful species across the Mediterranean.

## 6. Conclusion

North African populations are vulnerable to numerous ticks and tick-borne zoonoses. Populations in Europe are also increasingly vulnerable to North African ticks and tick-borne zoonoses due to a combination of climate change and the movement of ticks across the Mediterranean on migratory birds, human travellers, and trafficked wildlife. Therefore, a trans-national One Health approach is necessary to bring together researchers and policy makers from both European and North African countries to generate a significantly higher resolution understanding of the diversity, distribution, and ecology of ticks and zoonotic tick-borne pathogens in North Africa.

## Ethical approval

No formal ethical approval was needed.

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## Author contribution statement

**Abdelbaset Eweda Abdelbaset:** conceptualization, formal analysis, investigation, data curation, writing – original draft. **Mackenzie Kwak:** conceptualization, writing – review & editing. **Nariaki Nonaka:** resources, writing – review & editing. **Ryo Nakao:** conceptualization, writing – review & editing, supervision, funding acquisition. All authors read and approved the final manuscript.

## Declaration of Competing Interest

The authors declare they have no known competing interests.

## Data availability

No data was used for the research described in the article.

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