Abstract: Dromedary, or one-humped, camels *Camelus dromedarius* are an almost exclusively domesticated species that are common in arid areas as both beasts of burden and production animals for meat and milk. Currently, there are approximately 30 million dromedary camels, with highest numbers in Africa and the Middle East. The hardiness of camels in arid regions has made humans more dependent on them, especially as a stable protein source. Camels also carry and may transmit disease-causing agents to humans and other animals. The ability for camels to act as a point source or vector for disease is a concern due to increasing human demands for meat, lack of biosafety and biosecurity protocols in many regions, and a growth in the interface with wildlife as camel herds become sympatric with non-domestic species. We conducted a literature review of camel-borne zoonotic diseases and found that the majority of publications (65%) focused on Middle East respiratory syndrome (MERS), brucellosis, *Echinococcus granulosus*, and Rift Valley fever. The high fatality from MERS outbreaks during 2012–2016 elicited an immediate response from the research community as demonstrated by a surge of MERS-related publications. However, we contend that other camel-borne diseases such as *Yersinia pestis*, *Coxiella burnetii*, and Crimean–Congo hemorrhagic fever are just as important to include in surveillance efforts. Camel populations, particularly in sub-Saharan Africa, are increasing exponentially in response to prolonged droughts, and thus, the risk of zoonoses increases as well. In this review, we provide an overview of the major zoonotic diseases present in dromedary camels, their risk to humans, and recommendations to minimize spillover events.

Keywords: Camel, Nomadic, One health, Pathogen, Spillover, Zoonoses

INTRODUCTION

Worldwide there are roughly 30 million dromedary camels, with highest numbers found in Africa and the Middle East (Figure 1). Due to increased consumption and contact with camel meat and milk, camels represent a significant point source for zoonotic disease transmission to humans. Pastoralist camel production, in particular, is associated with a risk of disease spillover from wildlife into camel populations, and from camels to wildlife, as well as less opportunities for disease surveillance and control. By 2050 the human population is projected to grow by 2.5 billion, with nearly half of all population growth occurring in the African continent (Roser 2018). Along with the increase in human population in Africa and the Middle East, the camel population has also experienced steady growth as the de-
mand and production of camel meat and milk escalates (FAOSTAT 2016). More and more, nomadic herders are switching to an agricultural or urban setting to raise camels and this change in camel production brings potential risks of disease emergence and transmission. In addition, with the realities of climate change and the increase in drought conditions, camel hardiness has led to a shift in livestock choice in many regions of the world from cattle to camels, making camels even more abundant (Watson et al. 2016).

Limited resources, low levels of regulation, poor hygiene, high mobility of animals and herders, and lack of consistent veterinary care also act as drivers for disease spillover (Gossner et al. 2016; Megersa et al. 2011). Knowledge of camel-borne diseases, clinical signs, and pathways of transmission is thus important to mitigate human risks of camel-associated zoonoses. Many infectious diseases that have been an issue in Africa and the Middle East during the last decades, such as Middle East respiratory syndrome (MERS) and brucellosis, have an association with camel contact (Ahmed et al. 2010; Ferguson and Van Kerkhove 2014). Additionally, novel camel-borne diseases continue to be identified, as best exemplified by reports of a prion disease from Algerian abattoir camels published during the editing of this review paper (Babelhadj et al. 2018).

Significant research on seropositivity and detection of specific diseases of camels, those that have implications for human health, has been conducted; however, to the authors’ knowledge no publication has summarized the current literature on these zoonotic diseases. Realizing the need for a thorough review of the literature to identify the risks that camels pose to human health was the impetus for this review. In this paper, we review publications of the most common confirmed and potential camel zoonoses of interest: bacterial, viral, and parasitic, and offer recommendations for surveillance and control of the diseases of highest priority.

**METHODS**

We utilized two search engines, Google Scholar and PubMed, to search for publications related to camel-borne disease and zoonotic spillover. We chose Google Scholar for breadth and volume of content, while PubMed was chosen from medical and public health-specific search engines for its specificity. Publications on Bactrian camels *Camelus bactrianus* were excluded because they are primarily wild but are used as beasts of burden and food in select countries and only account for 2 million out of 30 million total camels (IUCN 2008). To cast a wide net for possible diseases we did not search for specific zoonotic diseases and instead classified publications by disease after the initial literature search. All search terms included the words camel and human as well as one of six other words: keywords: camel + human + zoonotic, illness, spillover, outbreak, transmission, or disease. For each set of search terms, we reviewed the first 100 results for relevancy or all results if < 100. Included publications were restricted to...
those written in English, but there was no date limit, no other restrictions were set, and papers were sorted by relevance. From a total of 1054 papers, 619 were unique or non-duplicates and 304 of these were relevant (Figure 2). Five of these 304 papers reported on multiple diseases. Results that were excluded included papers that inconclusively related to transmission from camels \( n = 96 \), non-camelid animals \( n = 40 \), studies that focused on vaccines \( n = 25 \), camel-specific diseases \( n = 22 \), articles/seminars \( n = 15 \), and non-relevant topics \( n = 117 \). Examples of non-relevance were papers that did not mention camels at all, papers that did not discuss transmission of disease, papers on human-to-human transmission, or papers that discussed laboratory testing and techniques related to these diseases. Food-borne bacterial diseases from pathogens such as *Escherichia coli*, *Salmonella*, and *Campylobacter* were consolidated into one category termed “food-borne” because they share transmission pathways, have similar symptoms, and were pre-grouped by several publications in this review. We also elected to present these pathogens in this fashion because there was a precedent set by said publications. Papers with positive serologic testing in camels, probable disease through an explained epidemiologic link between human disease and camel-borne pathogens, and isolation of similar strains in humans and camels fit criteria for inclusion. Relevant papers were sorted into bacterial, viral, and parasitic categories along with recorded counts for each disease. Results were separated out in this manner to cover scope number of diseases as well as depth number of papers per disease. Figures were created in Quantum GIS 3.6 (QGIS Development Team 2019). We completed the literature search in February and March of 2018.

**RESULTS**

Through this literature review, we identified 304 papers published between 1970 and 2018 that described disease agents in camels with probable (see above definition) or confirmed transmission to humans. Thirty-seven camel-borne diseases were identified, comprised of 12 bacterial diseases, 13 viral diseases, and 12 parasitic diseases (Table 1). The most frequently occurring diseases or disease-causing agents in this study were MERS \( n = 118 \), *Echinococcus granulosus* \( n = 46 \), brucellosis \( n = 35 \), and Rift Valley fever \( n = 19 \). In this study, 42 countries were represented in the literature, with most papers originating from Saudi Arabia \( n = 36 \), Iran \( n = 27 \), Kenya \( n = 15 \), and Egypt \( n = 14 \) (Figure 3). There has been a dramatic increase in publications over the last eight years with a peak during 2012–2016, when research on MERS was undertaken in a number of laboratories following the first diagnosis of a human fatality reported in 2012 (Fig. 4) (Kupferschmidt 2014).

![Figure 2. Methodology for inclusion and exclusion of publications of camel-borne zoonoses. Out of an initial 1054 eligible publications, 619 were unique and non-duplicate and 304 of those were included in the final selection of journal articles for further analysis](image-url)
| Disease/agent                          | Type          | Paper count | References                                                                                                                                 |
|---------------------------------------|---------------|-------------|-------------------------------------------------------------------------------------------------------------------------------------------|
| Middle East respiratory syndrome      | Virus         | 118         | Adney et al. (2014), Ahmed (2017a, b), Al Hammadi et al. (2015), Al salihi and Alrodhan (2017), Al-Tawfiq and Memish (2014a, b), Al-Tawfiq et al. (2014), Alagaili et al. (2014), Aleanizy et al. (2017), Alexandersen et al. (2014), Alhakeem et al. (2016), Alhamlan et al. (2017), Ali et al. (2017), Afraddadi et al. (2016), Alsolamy et al. (2017), Assiri et al. (2016), Azhar et al. (2014a, b), Balthy et al. (2016), Banik et al. (2015), Buchholz et al. (2013), Chan et al. (2014, 2015), Chu et al. (2014, 2015, 2018), Corman et al. (2014a, b, 2016), Cotten et al. (2013, 2014), Cramer et al. (2015), Deem et al. (2015), Devi et al. (2014), Drosten et al. (2015), Du and Han (2016), Dudas et al. (2018), Durai et al. (2015), Eckerle et al. (2014), El Bushra et al. (2016), Fanoy et al. (2014), Farag et al. (2015), Fehr et al. (2017), Ferguson and Van Kerkhove (2014), Food and Agriculture Organization of the United Nations (2017), Funk et al. (2016), Gardiner and MacIntyre (2014), Gossner et al. (2016), Gutiérrez et al. (2015), Haagmans et al. (2014, 2016), Han et al. (2016), Hemida et al. (2013, 2014, 2015, 2017), Holmes (2014), Hunter et al. (2016), Kayali and Peiris (2015), Khalafalla et al. (2015), Kupferschmidt (2015), Liljander et al. (2016), Mackay and Arden (2015, 2017), Majumder (2015), Memish et al. (2013, 2014a, b, 2015), Meyer et al. (2014, 2016), Miguel et al. (2016, 2017), Mohd et al. (2016), Muhairi et al. (2016), Müller et al. (2014, 2015), Ng et al. (2016), Nowotny and Kolodziejek (2014), Oladipo (2015), Olival and Epstein (2015), Omrani et al. (2015), Omrani and Shalhoub (2015), Park et al. (2015), Rabaan (2017), Raj et al. (2014), Rasmussen et al. (2015, 2016), Reeves et al. (2015), Reusken et al. (2013a, b, 2014a, b, 2015, 2016), Reuss et al. (2014), Sabir et al. (2016), Salkeld et al. (2016), Saqib et al. (2017), Shapiro et al. (2016), Sharif-Yakan and Kanj (2014), Shehata et al. (2016), Su et al. (2016), Tai et al. (2017), Watson et al. (2014), Wernery et al. (2015, 2016), Widagdo et al. (2016), de Wit et al. (2016), de Wit and Munster (2013), World Health Organization (2015), Younan et al. (2016), Yusof et al. (2015), Zhang et al. (2016), Zumba et al. (2015, 2016), Zumba and Memish (2014) |
| Hydatidosis                           | Parasite      | 46          | Abdel Aaty et al. (2012), Abushshewa et al. (2010), Ahmad (2005), Alvarez Rojas et al. (2014), Azab et al. (2004), Bardonnet et al. (2002, 2003), Casulli et al. (2010), Dinkel et al. (2004), Eckert and Deplazes (2004), Eckert et al. (1989), Elmahdi et al. (2004), Haillemariam et al. (2012), Hajialilo et al. (2012), Fasihi Harandi et al. (2002), Hassain et al. (2016), Kamenetzky et al. (2002), Karimi et al. (2017), Kia et al. (2010), Kinkar et al. (2017), Latif et al. (2010), Macpherson and McManus (1982), Macpherson and Smyth (1985), Maillard et al. (2006), Mandal and Deb Mandal (2012), McManus (1981), McManus and Rishi (1989), Mirzaei et al. (2016), Mobedi et al. (1970), Mrad et al. (2005), Oksanen and Lavikainen (2015), Omer et al. (2010a, b, Sadijadi (2006), Salem et al. (2011), Shahnazi et al. (2011), Shariatzehad et al. (2015), Sharma et al. (2013b), Singh et al. (2014), Spotin et al. (2015, 2017), Tigre et al. (2016), Thompson (2008), Utuk et al. (2008), Wachira et al. (1993), Youssef and Uga (2014), Zhang et al. (1998) |
| Disease/agent     | Type          | Paper count | References                                                                                                                                 |
|------------------|---------------|-------------|---------------------------------------------------------------------------------------------------------------------------------------------|
| Brucellosis      | Bacteria      | 35          | Abbas and Agab (2002), Ahmed et al. (2010), Al Dahouk et al. (2013), Bekele et al. (2013), Cooper (1992), Ducrottoy et al. (2015), El-Ansary et al. (2001), Fiori et al. (2000), Garcell et al. (2016), Gautret et al. (2013), Godfroid et al. (2005, 2013), Guumaa et al. (2014), Gwida et al. (2010, 2012), Kiel and Youssuf (1989), Megersa et al. (2011), Megersa et al. (2012), Memish and Balkhy (2004), Nimri (2003), Omer et al. 2010a, b, Osoro et al. (2015), Pappas (2010), Rhodes et al. (2016), Schelling et al. (2003), Schelling et al. (2004), Seleem et al. (2010), Shaalan et al. (2002), Shimol et al. (2012), Smits and Kadri (2005), Sprague et al. (2012), Teshome et al. (2003), Wernery (2014), Yahya (2015), Zewolda and Wereta (2012) |
| Rift Valley fever| Virus         | 19          | Abdo-Salem et al. (2006), Ahmed Kamal (2011), Bird et al. (2008), Britch et al. (2013), Chevalier et al. (2010), Chinikar et al. (2013), El Mamy et al. (2011, 2014), Faye et al. (2014), Gerdes (2004), Horton et al. (2014), Jäckel et al. (2013), Linthicum et al. (2016), Lutomiah et al. (2014), Merrill et al. (2015), Macharia et al. (2010), Paweska (2015), Swai and Sindato (2015), Weaver and Reisen (2010) |
| Food-borne       | Bacteria      | 15          | Dehkordi et al. (2013), Fadlelmula et al. (2016), Ghoneim et al. (2017), Hajialilo et al. (2012), Horton et al. (2014), Jaros et al. (2008), Kaindi et al. (2012), Rahimi et al. (2010, 2012), Rahimi and Kheirabadi (2012), Raufu et al. (2015), Salehi et al. (2012), Shabana et al. (2013), Sung et al. (2008), Tadesse (2015), Tejedor-Junco et al. (2015) |
| Plague (Yersinia pesta) | Bacteria      | 10          | Aikimbajev et al. (2003), Arbaji et al. (2005), Bramanti et al. (2016), Cabanel et al. (2013), Christie et al. (1980), Drancourt et al. (2006), El-Bahnasawy et al. (2012), Leslie et al. (2011), Saeed et al. (2005), Stenseth et al. (2008) |
| Camelpox         | Virus         | 9           | Balamurugan et al. (2013), Bera et al. (2010, 2011, 2015), Duraffour et al. (2011), Jezek et al. (1983), Khalafalla and Abdelazim (2017), Pearce-Duvet (2006), Shchelkunov (2013) |
| Q fever (Coxiella burnetii) | Bacteria      | 7           | Klemmer et al. (2018), Mohabbati Mobarez et al. (2017), Njeru et al. (2016), Pirouz et al. (2015), Schelling et al. (2003, 2004), Vanderburg et al. (2014) |
| Linguatula serrata | Parasite      | 7           | Bamarovat et al. (2014), Farjanikish and Shokrani (2016), Haddadzadeh et al. (2010), Oryan et al. (2011), Rezaei et al. (2012), Sadjjadi et al. (1998), Shakerian et al. (2008) |
| Hepatitis E      | Virus         | 5           | Khuroo and Khuroo (2016), Lee et al. (2016), Pavio et al. (2015), Rasche et al. (2016), Spahr et al. (2018) |
| Crimean–Congo hemorrhagic fever | Virus         | 4           | Champour et al. (2016), Khan et al. (1997), Mertens et al. (2013), Walker et al. (2016) |
| Tuberculosis     | Bacteria      | 4           | Cosivi et al. (1995), Garine-Wichatitsky et al. (2013), Gumi et al. (2012), Moda et al. (1996) |
| Anthrax          | Bacteria      | 3           | Aikembayev et al. (2010), Musa et al. (1993), Woods et al. (2004) |
| Trypanosoma evansi | Parasite      | 2           | Bennoune et al. (2013), Haridy et al. (2011) |
| Echthyma         | Virus         | 2           | Bazargani et al. (2010), Moallin and Zessin (1988) |
| Rotavirus        | Virus         | 2           | Ghosh et al. (2011), Jere et al. (2014) |
| Helminth         | Parasite      | 2           | Anvari-Tafti et al. (2013), McCarthy and Moore (2000) |
| Toxoplasmosis    | Parasite      | 2           | Alkazzaz (2013), Dekhordi et al. (2013) |
| Alkhurma hemorrhagic fever | Virus   | 1           | Carletti (2010) |
| Betacoronavirus   | Virus         | 1           | Woo et al. (2014) |
| UAE-HKU23        |               |             | |
| Dera Ghazi Khan virus | Virus       | 1           | Walker et al. (2016) |
| HCoV-229E        | Virus         | 1           | Corman et al. (2018) |
Viral

The large majority of publications were related to MERS, \( n = 118 \), a novel coronavirus. Genetic comparisons between camel and human isolated MERS are highly similar and camels continue to exhibit positive seropositivity for MERS in recent tests (Chu et al. 2018).

The review identified 19 papers on Rift Valley fever (RVF) transmission, most of which detailed how common seropositivity to RVF virus was in camel herds. Four of these papers emphasized that livestock like camels, cattle, and sheep served as important amplifiers for the virus, especially prior to outbreaks in Kenya and Mauritania (Bird et al. 2008; Britch et al. 2013; El Mamy et al. 2011, 2014).

Four of nine publications on Camelpox discussed human transmission, including a paper that reported the first laboratory-confirmed case of human Camelpox (Bera et al. 2011).

---

**Table 1.** continued

| Disease/agent | Type       | Paper count | References                      |
|---------------|------------|-------------|---------------------------------|
| Rabies        | Virus      | 1           | Bloch and Diallo (1995)         |
| Torque teno virus | Virus   | 1           | Al-Moslih et al. (2007)         |
| *Aeromonas spp.* | Bacteria  | 1           | Ghenghesh et al. (2001)         |
| *Bartonella*  | Bacteria   | 1           | Rasis et al. (2014)             |
| Glanders ("Burkholderia mallei") | Bacteria | 1           | Scholz et al. (2014)            |
| Johne’s disease (paratuberculosis) | Bacteria | 1           | Ghosh et al. (2012)             |
| *Klebsiella pneumoniae* | Bacteria | 1           | Kleinerman et al. (2013)        |
| Babesia bovis | Parasite   | 1           | Erekat et al. (2016)            |
| *Cryptosporidium* | Parasite | 1           | Saizmand et al. (2012)          |
| Fascioliasis | Parasite   | 1           | Younan et al. (2016)            |
| Leishmaniosis | Parasite   | 1           | Ashford (2000)                  |
| Onchocerciasis | Parasite   | 1           | El-Bahnasawy et al. (2015)      |
| Sarcocystis | Parasite   | 1           | Chhabra and Samantaray (2012)    |
| Trichinelliosis | Parasite | 1           | Bommer et al. (1980)            |

**Figure 3.** Number of publications by country of study, range \( n = 1 \) Finland, Argentina to \( n = 36 \) Saudi Arabia
There were five papers on hepatitis E, one of the five known human hepatitis virus strains, in which camel meat and milk were implicated as risk factors in humans through whole-genome sequencing, HEV IgM, or HEV RNA detection (Pavio et al. 2015; Khuroo and Khuroo 2016; Lee et al. 2016; Rasche et al. 2016; Spahr et al. 2018). In one of these reports, a liver transplant patient in the United Arab Emirates consumed camel meat and milk regularly and was chronically infected with hepatitis E (Lee et al. 2016).

While no publication documented clinical evidence of camel–human rabies transmission, one paper presented probable evidence of camel-to-human rabies transmission (Bloch and Diallo 1995). A 2018 publication noted that HCoV-229E, a primarily non-lethal coronavirus responsible for a proportion of upper and lower respiratory tract infections, can be transmitted from camels to humans similar to MERS transmission, thus implicating dromedary camels as a possible reservoir of coronaviruses (Corman et al. 2018). Woo et al. (2014) identified a novel betacoronavirus UAE-HKU23 or dromedary camel coronavirus DcCOV in the United Arab Emirates that was detected in 52% of tested camel serum samples.

Other viruses that were found in camels include Alkhurma hemorrhagic fever (AHF) virus \( n = 1 \), Crimean–Congo hemorrhagic fever (CCHF) virus \( n = 4 \), rotavirus \( n = 2 \), camel contagious ecthyma \( n = 2 \), torque teno virus \( n = 1 \), and Dera Ghazi Khan virus \( n = 1 \) (Moallin and Zessin 1988; Khan et al. 1997; Al-Moslih et al. 2007; Bazzargani et al. 2010; Carletti 2010; Ghosh et al. 2011; Horton et al. 2014; Jere et al. 2014; Champour et al. 2016; Walker et al. 2016).

**Bacterial**

A total of 35 papers discussed the risk of brucellosis as a public health threat from camels. Most of these 35 papers (18; 51%) were seroprevalence studies of brucellosis in camels, which reported a prevalence range of between 1.4 and 37.5% (Schelling et al. 2004; Omer et al. 2010a, b).

Bacterial diseases that are transmitted through food, water, or other types of fecal–oral transmission were grouped together as “food-borne.” This group included *Salmonella*, *E. coli*, *Helicobacter*, *Staphylococcus*, *Enterococci*, *Campylobacter*, and *Leptospirosis*. These diarrheal bacteria were reported in 15 papers, four of which discussed testing for antimicrobial resistance in camels and camel products (Rahimi et al. 2010; Tadesse 2015; Tejedor-Junco et al. 2015; Fadlelmula et al. 2016).

Ten papers described camel transmission of plague, *Yersinia pestis*. In fact, three papers documented plague infection in patients who directly consumed raw camel
meat (Christie et al. 1980; Arbaji et al. 2005; Cabanel et al. 2013).

Seven papers detailed high Q fever *Coxiella burnetii* seropositivity in camels (Schelling et al. 2003; Schelling et al. 2004; Vanderburg et al. 2014; Pirouz et al. 2015; Njeru et al. 2016; Mohabbati Mobarez et al. 2017; Klemmer et al. 2018). Seroprevalence levels of up to 73% were present in camels in Chad (Schelling et al. 2004). Humans that work in close contact with camels such as herders, farmers, and breeders are especially at risk of Q fever transmission, with one study finding a high odds ratio (OR = 9) for the association of being a camel breeder and Q fever seropositivity (Schelling et al. 2003).

The four papers on camel tuberculosis all discussed positive detection of *M. bovis*, indicating that camels are likely also a reservoir for human transmission (Cosivi et al. 1995; Moda et al. 1996; Gumi et al. 2012; Garine-Wichatitsky et al. 2013). Gumi et al. (2012) found isolated *M. tuberculosis* from camels and *M. bovis* from humans, which suggests cross-species transmission of both strains of bacteria.

One of three papers on anthrax conclusively extracted anthrax spores from infected camel meat, which led to illness in ten people (Musa et al. 1993).

Other bacterial diseases in the literature but occurring less frequently included *Rickettsia aeschlimannii* 1, *Klebsiella pneumoniae* 1, *Aeromonas spp.* 1, *Bartonella spp.* 1, *Burkholderia mallei* 1, and *M. avium subsp. paratuberculosis* 1 (Genghesh et al. 2001; Ghosh et al. 2012; Kleinerman et al. 2013; Sharma et al. 2013a, b; Rasis et al. 2014; Scholz et al. 2014).

Parasitic

The most common zoonotic parasite transmitted from camels to humans was *Echinococcus granulosus* n = 46. This parasite has a variety of hosts but is often found in livestock as intermediate hosts, including camels. A review by Alavrez Rojas et al. (2014) estimated that the camel strain of *E. granulosus* causes between 7 and 11% of all hydatid infections in humans. This attributable risk estimate likely varies by geographic location; a molecular survey by Omar et al. (2010a, b) found that 59% of camels in Sudan were infected with *E. granulosus*, and a subsequent Sudanese paper found that camels and cattle were the principal intermediate host, not sheep as previously believed (Elmahdi et al. 2004).

There were two papers on the parasite *Trypanosoma evansi*. Prevalence rates of up to 14% were found in camels in Algeria which is comparatively high to other countries and increases risk for human transmission (Benoune et al. 2013). Human cases, confirmed with ELISA and stained blood films, of *T. evansi* have been reported in India and Egypt (Haridy et al. 2011).

Parasitic diseases are commonly passed from camels to humans through meat and milk consumption. One paper on a trichinellosis outbreak in Germany detailed how camel meat brought from Egypt was responsible for zoonotic transmission (Bommer et al. 1980), and in 2013, researchers detected *Toxoplasma gondii* in camel milk (Dehkordi et al. 2013). Other fecal- and meat-/milk-transmitted parasites included *Leishmania* spp. n = 1, *Babesia bovis* n = 1, *Cryptosporidium* spp. n = 1, and *Sarcocystis* spp. n = 1 (Ashford 2000; Szamand et al. 2012; Chhabra and Samantary 2012; Ereqat et al. 2016). Four other parasite species found in this cohort were helminths *Haemonchus tataricus*, *Trichostrongylus hamatus*, and *Trichuris infundibulius* n = 2; *Linguatula serrata* n = 7; *Onchocerca volvulus* n = 1; and *Fasciola hepatica* or *Fasciola gigantica* n = 1 (Sadjjadi et al. 1998; McCarthy and Moore 2000; Shakerian et al. 2008; Haddadzadeh et al. 2010; Oryan et al. 2011; Rezaei et al. 2012; Anvari-Tafiti et al. 2013; Bamorovat et al. 2014; Youssef and Uga 2014; El-Bahna-sawy et al. 2015; Farjanikish and Shokrani 2016).

**DISCUSSION**

As determined by publication count as well as known mortality rates, viruses in this review are of highest interest, followed by bacteria and parasites (Table 1). Camels are as ubiquitous as cattle or sheep in many parts of the world; yet, knowledge on potential health risks lags behind that of other livestock species. The combination of human-related climate change, population growth, decline in biodiversity, and land-use change are major drivers for the evolution and spread of zoonotic disease (Engering et al. 2013).

The emergence of MERS, with outbreaks between 2012 and 2016, was an outcome of these realities, and it is no surprise that MERS continues to receive high amounts of publicity and funding due to its high human fatality rates ~35% and pandemic potential (World Health Organization 2017). There are currently no widely used vaccines against MERS, but knowledge of its transmission is critical to better implement food safety and sanitation practices.
within the camel value chain. Rift Valley fever (RVF) was the second most common camel-borne zoonosis in this review and is not a significant source of mortality as less than 3% of patients develop lethal symptoms. However, it is a significant cause of morbidity especially in high-risk populations such as veterinarians, butchers, scientists, animal health workers, farmers, and herders (Ikekami and Makino 2011). The same goes for Camelpox, which is a minor health problem for camel farmers but incurs significant economic damages from the death of young camels, reduced milk yield, and lasting morbidity (Balamurugan et al. 2013). MERS, RVF, and Camelpox were some of the most commonly reported camel-borne zoonotic viruses in this literature review, but for preventive purposes awareness of the following viruses is important to promote. Crimean–Congo hemorrhagic fever is listed as a disease with epidemic potential due to its high mortality rate, growing prevalence in Asia and Europe, and lack of vaccines (Mertens et al. 2013). Alkhurma hemorrhagic fever (AHF) is also a disease of interest because of its hemorrhagic symptoms, recent emergence, and lack of detailed knowledge of its symptoms and transmission. Mortality rates for these viruses along with other hemorrhagic fevers are high because of difficulties in disease diagnosis (World Health Organization 2016). Alkhurma hemorrhagic fever, CCHF, and Dera Ghazi Khan are mosquito- and tick-borne diseases where camels act as reservoirs and amplifiers (Carletti 2010; Walker et al. 2016). Thus, vector surveillance and management around camels in addition to the aforementioned sanitation practices could be highly beneficial to control the spread of these diseases.

The bacterial disease of greatest concern is brucellosis, which is not only zoonotic but also causes severe economic losses for farmers and ranchers across the world in lost milk, reduced fertility, stillbirths, and abortions (Akakpo et al. 2010). Camel farmers should be cautious and aware when handling camels, and this exemplifies another area where increased attention to sanitation practices would be beneficial. Food-borne diseases are of high importance as evidenced by the rapid establishment of complex camel milk value chains in urban Kenya as well as the breadth of food-borne pathogens found in our review (Muloii et al. 2018). These locations exemplify the high-risk transmission interfaces that are formed due to a lack of proper protocol and oversight by government agencies in regard to food safety training and hygienic practices (Muloii et al. 2018). Camels contract plague from infected fleas and may infect humans through contact with infected bodily fluids or consumption of infected meat (Leslie et al. 2011). However, vaccination in humans can be used to control the spread and occurrence of outbreaks. For example, vaccination rates have steadily increased in Kazakhstan since 2001 and the usage of vaccines in combination with antibiotics has greatly reduced case fatality across the country (Aikimbajev et al. 2003). The abundance of publications on brucellosis, plague, and food-borne bacterial illnesses reaffirms their presence in camels.

The earliest papers in this review came from the 1970s and almost exclusively discussed parasitic diseases like E. granulosus with occasional papers on viral and bacterial disease. This finding is consistent with a historical lack of widespread high-quality technology for viral and bacterial detection, as well as increased focus on viruses today as compared to 30–40 years ago. Parasitic diseases in this review were not significant sources of mortality. Cysts from E. granulosus occur on lung and liver tissue along with other internal organs and contribute to morbidity in humans through pressure effects and problematic locations of cysts (Mandal and Deb Mandal 2012). Vaccination of camels against E. granulosus is not widely practiced because sheep and dogs are considered to be more important hosts: This, in combination with unsanitary practices and high camel and sheep densities, creates higher risk for humans in these areas (Zhang and McManus 2006). No other publications on parasites showed that they were significant sources of human mortality, and there were low paper counts for most parasites, which could indicate their rarity in camels and largely non-lethal status.

Many studies demonstrated a high seroprevalence to a variety of zoonotic pathogens in camel populations along with current or past examples of camel–human transmission. However, few validated standardized tests exist for camels, making disease detection and confirmation difficult (Gwida et al. 2011). Seropositivity is an indication of antibodies and not antigens, so while this shows that a camel was exposed, it does not provide information on the infection status of the individual or the ability of the camel to transmit a pathogen. These papers may not have exact confirmation for each strain in each country or population, but high prevalence coupled with known instances of transmission provides a guideline for prospective risks. Additionally, because we did not analyze our results with statistical methods we were unable to assess the strength of association between pathogens and human risk. Another limitation of our review was the absence of certain pivotal papers; this may have been due to the use of Google Scholar
as one of the two major search engines. A serosurvey of Q fever in Laikipia County, Kenya, that revealed high seroprevalence 18.6% in dromedaries was one such paper that fit our inclusion and search criteria keywords: camel, zoonotic, human, but did not appear in any searches (Browne et al. 2017). A common critique of Google Scholar is the limited ability to sort results, which thus provides evidence that it misses important literature in many case studies (Haddaway et al. 2015). Although we did use PubMed we still may have missed eligible publications because of relevance sorting and/or using only the first 100 results. Our study was limited to peer-reviewed material in English and excludes a thorough review of French, Turkish, Farsi, and Arabic literature which could have provided more information in target regions. The use of additional search engines or search terms may improve the scope of literature reviews, which we will make note of for the future.

Lastly, a limitation not necessary related to methodology but rather the epidemiology of diseases relates to missing diseases at the camel–other livestock/wildlife–human interface that we would not have captured in our review. Although we did not include them as part of this review there were papers found in our initial searches that described camel–livestock and camel–wildlife transmission. These shared pathogens may be zoonotic and include camels as part of the transmission cycle but are not necessarily identified as a camel-borne zoonosis. For example, other animals may be the original or primary source of many pathogens, such as the case of MERS in bats, with the camel being an intermediate host in the transmission from animal to human (Corman et al. 2014a, b).

Dromedary camels are a staple in the diets and lives of humans like their cattle and pig counterparts, but research on their zoonotic disease potential is lacking in comparison. When the map of camel population density is compared to the geographic site of published papers found in this review, we see that the two have high levels of intersection in Africa, Asia, and the Middle East (Figures 1 and 3). However, these maps also show that in many instances camel-borne zoonoses are not restricted to areas of high camel numbers and human infections can and do occur in countries with very low camel populations, and even in countries with no camels as a person may be exposed in one region and travel to another. Therefore, veterinarians, farmers, and others working in close contact with camels and camel products should be cognizant of these potential pathogens, not just in areas where camels are raised but also where camel products may be processed and transported. Additionally, physicians must be aware of where their patients have traveled. Knowledge of potential camel-borne diseases is thus important for researchers and health workers to consider globally.

**CONCLUSION**

Camels are not common outside of hot and arid areas such as sub-Saharan Africa or the Middle East, but knowledge of their potential carrier status is important to researchers, zoo personnel, and travelers. The MERS and Ebola outbreaks in recent years have shown how rapidly pathogens can travel and erupt in novel human populations; population expansion and a lack of extensive healthcare systems make camel-endemic areas a potential hot spot for zoonotic spillover. Many of the zoonotic pathogens of camels are a current or possible future risk to human health and must be considered by medical professionals, especially in light of the increased use of camels as a growing protein source globally. As we collect epidemiologic data on the routes of transmission and sources of these infectious agents, we become better prepared to manage and mitigate their impact on humans. Camel milk and meat act as a point source for infection and should be managed with proper slaughter protocols, pasteurization, and improved overall sanitation practices. Dromedary camels also act as a significant source and amplifier for vector-borne disease; therefore, vaccination of camels, control of mosquitoes and ticks, insecticide application, and consistent screening will help control infection rates in camels and humans. In this literature review, we highlight a number of camel-borne zoonotic diseases. The number of pathogens and spillover events will most likely continue to grow as human and camel populations increase and increasingly intersect.

**ACKNOWLEDGEMENTS**

This work was made possible by the generous support of the American people through the United States Agency for International Development (USAID) Emerging Pandemic Threats PREDICT Cooperative Agreement No. AID-OAA-A-14-00102. The contents are the responsibility of the authors and do not necessarily reflect the views or the policy of USAID or the US Government, and no official endorsement should be inferred. Thank you to Smithsonian Conservation Biology Institute and Saint Louis Zoo.
Institute for Conservation Medicine for additional funding to complete this research. Special thanks to our fellow camel researchers and their contributions over the years.

COMPLIANCE WITH ETHICAL STANDARDS

CONFLICT OF INTEREST The authors declare that they have no conflict of interest.

REFERENCES

Abbas B, Agab H (2002) A review of camel brucellosis. Prev Vet Med 55:47–56. https://doi.org/10.1016/S0167-5877(02)00055-7

Abdel Aaty HE, Abdel-Hameed DM, Alam-Eldin YH, El-Shennawy SF, Aminou HA, Makled SS, Darweesh SK (2012) Molecular genotyping of Echinococcus granulosus in animal and human isolates from Egypt. Acta Trop 121:125–128. https://doi.org/10.1016/j.actatropica.2011.10.014

Abdo-Salem S, Gerbier G, Bonnet P, Al-Qadasi M, Tran A, Thiry E, Al-Eriny G, Roger F (2006) Descriptive and spatial epidemiology of Rift Valley fever outbreak in Yemen 2000–2001. Ann N Y Acad Sci 1081:240–242. https://doi.org/10.1196/annals.1373.028

Abushewa MH, Abushhiwa MHS, Nolan MJ, Jex AR, Campbell MN, Keim P, Francesconi SC, Blackburn JK, Hugh-Jones M, T, Pazylov Y, Zakaryan S, Denissov G, Easterday WR, Van Ert BE, Jabbar A, Gasser RB (2010) Genetic classification of Echinococcus granulosus cysts from humans, cattle and camels in Libya using mutation scanning-based analysis of mitochondrial loci. Mol Cell Probes 24:346–351. https://doi.org/10.1016/j.mcp.2010.07.005

Adney DR, van Doremalen N, Brown VR, Bushmaker T, Scott D, de Wit E, Bowen RA, Munster VJ (2014) Replication and Shedding of MERS-CoV in upper respiratory tract of inoculated dromedary camels. Emerg Infect Dis 20:1999–2005. https://doi.org/10.3201/eid2012.141280

Ahmadi NA (2005) Hydatidosis in camels Camelus dromedarius and their potential role in the epidemiology of Echinococcus granulosus in Iran. J Helminthol 79:119–125. https://doi.org/10.1079/JOH2005279

Ahmed AE (2017) Diagnostic delays in 537 symptomatic cases of Middle East respiratory coronavirus infection in Saudi Arabia. Int J Infect Dis 62:47–51. https://doi.org/10.1016/j.ijid.2017.07.008

Ahmed AE (2017) The predictors of 3- and 30-day mortality in 660 MERS-CoV patients. BMC Infect Dis. https://doi.org/10.1186/s12879-017-2127-2

Ahmed Kamal S (2011) Observations on Rift Valley fever virus and vaccines in Egypt. Virol J 8:532. https://doi.org/10.1186/1743-422X-8-532

Ahmed MO, Elmehri SE, Abuzweda AR, Blauo M, Abouzeed YM, Ibrahim A, Salem H, Alzwmam F, Abid S, Elahem A, Elrais A (2010) Seroprevalence of brucellosis in animals and human populations in the western mountains region in Libya, December 2006-January 2008. Euro Surveill 15:30

Aikembayev AM, Lukhnova L, Temiralieyeva G, Meka-Mechenko T, Pazylow Y, Zakaryan S, Denissov G, Easterday WR, Van Ert MN, Keim P, Francesconi SC, Blackburn JK, Hugh-Jones M, Hadfield T (2010) Historical Distribution and Molecular Diversity of Bacillus anthracis, Kazakhstan. Emerg Infect Dis 16:789–796. https://doi.org/10.3201/eid1605.091427

Aikimbajev A, Meka-Mechenko T, Temiralieva G, Bekenov J, Sagiyev Z, Kaljan K, Mukhambetova AK (2003) Plague in Kazakhstan at the present time. Przegl Epidemiol 57:593–598

Akakpo A, Teko-Agbo A, Koné P 2010 The impact of brucellosis on the economy and public health in Africa. In: Compendium of technical items presented to the OIE World Assembly of Delegates or to OIE Regional Commissions, vol 2009, pp 71–84.

Al Dahouk S, Sprague LD, Neubauer H (2013) New developments in the diagnostic procedures for zoonic brucellosis in humans. Revue Scientifique Et Technique International Office of Epizootics 32:177–188

Al Hammadi ZM, Chu D KW, Eltahir YM, Al Hosani F, Al Mulla M, Tarmini W, Halil AJ, Perera RAPM, Abdelkalek MM, Peiris JSM, Al Muhiari SS, Poon LLM (2015) Asymptomatic MERS-CoV infection in humans possibly linked to infected dromedaries imported from Oman to United Arab Emirates, May 2015. Emerg Infect Dis 21:2197–2200. https://doi.org/10.3201/eid2111.151132

Al-Moslih MI, Perkins H, Hu Y-W (2007) Genetic relationship of Toxoplasma gondii TTV between humans and camels in United Arab Emirates UAE. J Med Virol 79:188–191. https://doi.org/10.1002/jmv.20776

Al salihi SF, Alrodhan M (2017) Phylogenetic analysis of MERS-CoV in human and camels in Iraq. Int J Pharm Res Allied Sci 6:120–129

Al-Tawfiq J, Memish ZA (2014) Middle East respiratory syndrome coronavirus: epidemiology and disease control measures. Infect Drug Resist. https://doi.org/10.2147/ird-s51283

Al-Tawfiq J, Memish ZA (2014) Middle East respiratory syndrome coronavirus: transmission and phylogenetic evolution. Trends Microbiol 22:573–579. https://doi.org/10.1016/j.tim.2014.08.001

Al-Tawfiq J, Zumla A, Memish ZA (2014) Travel implications of emerging coronaviruses: SARS and MERS-CoV. Travel Med Infect Disease 12:422–428. https://doi.org/10.1016/j.tmaid.2014.06.007

Alagaili AN, Briese T, Misbra N, Kapoor V, Sameroff SC, de Wit E, Munster VJ, Hensley LE, Zalmout IS, Kapoor A, Epstein JH, Karesh WB, Daszak P, Mohammed OB, Lipkin WI (2014) Middle East respiratory syndrome coronavirus infection in dromedary camels in Saudi Arabia. mbio. https://doi.org/10.1128/mbio.00884-14

Alnaza AD (2013) Determination of Seropositivity for Toxoplasma gondii in Sheep, Goats and Camels Slaughtered for Food and Human Consumptions in Riyadh Municipal Abattoirs, Saudi Arabia. J Egypt Soc Parasitol 43:569–576. https://doi.org/10.12816/0006414

Aleanizy FS, Midgley CM, Assiri AM, Alessa M, Al Hawaj H, Saeed AB, Almasri MM, Lu X, Abedi GR, Abdalla O, Mohammed M, Algarni HS, Al-Abdely HM, Alsharief AA, Nooh R, Erdman DD, Gerbier SI, Watson JT (2016) Exposures among MERS Case-Patients, Saudi Arabia, January–February 2016.
Dromedary Camels: A Literature Review
Fadlelmula A, Al-Hamam NA, Al-Dugaym AM (2016) A potential camel reservoir for extended-spectrum \beta-lactamase-producing \textit{Escherichia coli} causing human infection in Saudi Arabia. \textit{Trop Anim Health Prod} 48:427–433. https://doi.org/10.1007/s11250-015-0970-9

Fanoy EB, van der Sande MA, Kraaij-Dirkzwager M, Dirksen K, Jonges M, van der Hoek W, Koopmans MP, der Werf D, Sonder G, van der Weijden C, de Heuvel J, Gelincik L, Bouwhuis JW, van Gageldonk-Lafeber ABon behalf of the members of the MERS-CoV outbreak investigation team of The Netherlands (2014) Travel-related MERS-CoV cases: an assessment of exposures and risk factors in a group of Dutch travellers returning from the Kingdom of Saudi Arabia, May 2014. \textit{Emerg Themes Epidemiol} 11:16. https://doi.org/10.1186/1742-7622-11-16

Farag EABA, Reusken CBEM, Haagmans BL, Mohran KA, Raj VS, Pas SD, Voermans J, Smits SL, Godeke G-J, Al-Hajri MM, Al-hajri FH, Al-Romaihi HE, Gobashy H, El-Maghraby MM, El-Sayed AM, Al Thani MHJ, Al-Marri S, Koopmans MPG (2015) High proportion of MERS-CoV shedding dromedaries at slaughterhouse with a potential epidemiological link to human cases, Qatar 2014. \textit{Infect Ecol Epidemiol} 5:28305. https://doi.org/10.3402/iee.v5.28305

Farjanikish G, Shokrani H (2016) Prevalence and morphopathological characteristics of linguatulosis in one-humped camel \textit{Camelus dromedarius} in Yazd, Iran. \textit{Parasitol Res} 115:3163–3167. https://doi.org/10.1007/s00436-016-5074-6

Faye O, Ba H, Ba Y, Freire CCM, Faye O, Ndaiye O, Elgaday IO, Zanotto PMA, Diaolo M, Sall AA (2014) Reemergence of Rift Valley fever, Mauritania, 2010. \textit{Emerg Infect Dis} 20:300–303. https://doi.org/10.3201/eid2005.130996

Fehr AR, Channappanavar R, Perlman S (2017) Middle East respiratory syndrome: emergence of a pathogenic human coronavirus. \textit{Annu Rev Med} 68:387–399. https://doi.org/10.1146/annurev-med-051215-031152

Ferguson NM, Van Kerkhove MD (2014) Identification of MERS-CoV in dromedary camels. \textit{Lancet Infect Dis} 14:93–94. https://doi.org/10.1016/S1473-3099(13)70691-1

Fiori PL, Mastrandrea S, Rappelli P, Cappuccinelli P (2000) Brucella abortus infection acquired in microbiology laboratories. \textit{J Clin Microbiol} 38:2005–2006

Food and Agriculture Organization of the United Nations FAO (2017) Human exposure to Middle East respiratory syndrome coronavirus from livestock or wildlife species August 2017. FAO Animal Health Risk Analysis—Assessment, Issue No. 4. Rome, FAO

FAOSTAT (2016) Food and agriculture organization corporate statistical database. http://www.fao.org/faostat/en/#data. Accessed 12 April 2018

Funk AL, Goutard FL, Miguel E, Bourgarel M, Chevalier V, Faye B, Peiris JSM, Van Kerkhove MD, Roger FL (2016) MERS-CoV at the animal–human interface: inputs on exposure pathways from an expert-opinion elicitation. \textit{Front Vet Sci}. doi.org/10.3389/fvets.2016.00088

Garcell HG, Garcia EG, Puyou PV, Martin IR, Arias AV, Alfonso Serrano RN (2016) Outbreaks of brucellosis related to the consumption of unpasteurized camel milk. \textit{J Infect Public Health} 9:523–527. https://doi.org/10.1016/j.jiph.2015.12.006

Gardner LM, MacIntyre C (2014) Unanswered questions about the Middle East respiratory syndrome coronavirus MERS-CoV. \textit{BMC Res Notes} 7:358. https://doi.org/10.1186/1756-0500-7-358

Garine-Wichatisky MD, Caron A, Kock R, Tschopp R, Munyembe M, Hofmeyr M, Michel A (2013) A review of bovine tuberculosis at the livestock–human interface in sub-Saharan Africa. \textit{Epidemiol Infect} 141:1342–1356. https://doi.org/10.1017/S0950268813000708

Gautret P, Benkouiten S, Gaillard C, Parola P, Brouqui P (2013) Camel milk-associated infection risk perception and knowledge in French Hajj Pilgrims. \textit{Vector Borne Zoonotic Dis} 13:425–427. https://doi.org/10.1089/vbz.2012.1010

Gerdes GH (2004) Rift Valley fever. \textit{Revue scientifique et technique Int Off Epizoot} 23:613–624

Ghenghesh KS, El-Ghodban A, Dkakni R, Abeid S, Altoni A, Abdussalam T, Marialigeti K (2001) Prevalence, species differentiation, haemolytic activity, and antibiotic susceptibility of aeromonads in untreated well water. \textit{Memórias do Instituto Oswaldo Cruz} 96:169–173. https://doi.org/10.1590/S0074-02762001000200006

Ghoneim NH, Abdel-Moein KA, Zaher H (2017) Camel as a transboundary vector for emerging exotic \textit{Salmonella} serovars. \textit{Pathog Glob Health} 111:143–147. https://doi.org/10.1080/20477724.2017.1309343

Ghosh S, Gatheru Z, Nyangao J, Adachi N, Urushibara N, Kobayashi N (2011) Full genomic analysis of a G8[P1] rotavirus strain isolated from an asymptomatic infant in Kenya provides evidence for an artiodactyl-to-human interspecies transmission event. \textit{J Med Virol} 83:367–376. https://doi.org/10.1002/jmv.21974

Ghosh P, Hsu C, Alyamani EJ, Shehata MM, Al-Dubaib MA, Al-Naem A, Hashad M, Mahmoud OM, Alharbi KBJ, Al-Busadah K, Al-Swailem AM, Talaat AM (2012) Genome-wide analysis of the emerging infection with mycobacterium avium subspecies paratuberculosis in the Arabian Camels \textit{Camelus dromedarius}. \textit{PLoS ONE} 7:e31947. https://doi.org/10.1371/journal.pone.0031947

Godfroid J, Cloeckaert A, Liautard J-P, Kohler S, Fretin D, Wallravens K, Garin-Bastuji B, Letesson J-J (2005) From the discovery of the Malta fever’s agent to the discovery of a marine mammal reservoir, brucellosis has continuously been a re-emerging zoonosis \textit{Vet Res} 36:313–326. https://doi.org/10.1051/vetres:2005003

Godfroid J, Al Dahouk S, Pappas G, Roth F, Matege G, Muma J, Marcotty T, Pfeiffer D, Skjerve E (2013) “One Health” surveillance and control of brucellosis in developing countries: moving away from improvisation. \textit{Comp Immunol Microbiol Infect Dis} 36:241–248. https://doi.org/10.1016/j.cimid.2012.09.001

Gossner C, Danielson N, Gervelmeyer A, Berthe F, Faye B, Kaask Aaslav K, Adlhoch C, Zeller H, Penttinen P, Coulombier D (2004) Rift Valley fever. \textit{Revue Scientifique Et Technique Int Off Epizoot} 33:957–996

Gumaa MM, Osman HM, Omer MM, El Sanousi EM, Godfroid J, Al-Swailem AM, Talaat AM (2012) Genome-wide analysis of the emerging infection with mycobacterium avium subspecies paratuberculosis in the Arabian Camels \textit{Camelus dromedarius}. \textit{Comp Immunol Microbiol Infect Dis} 36:241–248. https://doi.org/10.1016/j.cimid.2012.09.001

Gumai B, Schelling E, Berg S, Firdessa R, Erenso G, Mekonnen W, Hailu E, Melese E, Hussein J, Aseffa A, Zinsstag J (2012) Zoonotic transmission of tuberculosis between pastoralists and their
livestock in South–East Asia. EcoHealth 9:139–149. https://doi.org/10.1007/s10393-012-0754-x

Gutiérrez C, Tejedor-Junco MT, González M, Lattwein E, Reneker S (2015) Presence of antibodies but no evidence for circulation of MERS-CoV in dromedaries on the Canary Islands, 2015. Eurosurveillance. https://doi.org/10.2807/1560-7917.es.2015.20.37.30019

Gwida M, Al Dahouk S, Melzer F, Rössler U, Neubauer H, Tomas H (2010) Brucellosis: regionally emerging zoonotic disease? Croat Med J 51:289–295. https://doi.org/10.3325/cmj.2010.51.289

Gwida M, El-Gohary A, Melzer F, Khan I, Rössler U, Neubauer H (2012) Brucellosis in camels. Res Vet Sci 92:351–355. https://doi.org/10.1016/j.rvsc.2011.05.002

Gwida MM, El-Gohary AH, Melzer F, Tomas H, Rosler U,ternery U, Wernery R, Elschner MC, Khan I, Eickhoff M, Schoner D, Neubauer H (2011) Comparison of diagnostic tests for the detection of Brucella spp. in camel sera. BMC Res Notes 4:525. https://doi.org/10.1186/1756-0500-4-525

Haagmans BL, Al Dahairy SHS, Reusken CBEM, Raj VS, Galiano MPG (2014) Middle East respiratory syndrome coronavirus in dromedary camels: an outbreak investigation. Lancet Infect Dis 14:140–145. https://doi.org/10.1016/S1473-3099(13)70960-X

Haagmans BL, van den Brand JMA, Raj VS, Volk A, Wohlschin P, Smits SL, Schipper D, Bestebroer TM, Okba N, Fux R, Bensaid H, Solanes Foz D, Kuiken T, Baumgartner W, Segales J, Sutter RK, Cogger N, French N (2008) A systematic review of the giardiasis transmission of Middle East respiratory syndrome coronavirus in dromedary camels. Science 321:525. https://doi.org/10.1126/science.1162183

Haddadzadeh HR, Athari SS, Abedini R, Khazraii Nia S, Khazraii nia P, Nabian S, Haji-Mohamadi B (2010) One-humped camel Camels dromedarius infection with Linguatula serrata in Tabriz, Iran. Iran J Arthropod-Borne Dis 4:54–59

Haddaway NR, Collins AM, Coughlin D, Kirk S (2015) The role of google scholar in evidence reviews and its applicability to grey literature searching. PLoS ONE 10:e0138237. https://doi.org/10.1371/journal.pone.0138237

Hailemariam Z, Nakao M, Menkir S, Lavikainen A, Yanagida T, Gwida M, El-Gohary A, Melzer F, Khan I, Sutter RK, Osterhaus ADME, AllHajri FM, El-Metwally MT, Khalil HH, Morsy TA (2011) Trypanosoma evansi in dromedary camel: with a case report of zoonosis in greater Cairo, Egypt. J Egypt Soc Parasitol 41:85–76

Hassanain MA, Shaapan RM, Khalil FAM (2016) Sero-epidemiological value of some hydatid cyst antigen in diagnosis of human cystic echinococcosis. J Parasit Dis 40:52–56. https://doi.org/10.1007/s12639-014-0443-5

Hemida MG, Al-Naeem A, Perera RAPM, Chinn AWH, Poon LLM, Peiris M (2015) Lack of Middle East respiratory syndrome coronavirus transmission from infected camels. Emerg Infect Dis 21:699–701. https://doi.org/10.3201/eid2014.141949

Hemida MG, Chu DKW, Poon LLM, Perera RAPM, Alhammadi MA, Ng H, Siu LY, Guan Y, Alnæem A, Peiris M (2014) MERS coronavirus in dromedary camel Herd, Saudi Arabia. Emerg Infect Dis. https://doi.org/10.1371/journal.pone.0138237

Hemida MG, Elmoslemany A, Al-Hizab F, Alnæem A, Almamam F, Faye B, Chu DKW, Perera RAPM, Peiris M (2017) Dromedary camels and the transmission of Middle East respiratory syndrome coronavirus MERS-CoV. Transbound Emerg Dis 64:344–353. https://doi.org/10.1111/tbed.12401

Hemida M, Perera R, Wang P, Alhammadi M, Siu L, Li M, Poon L, Saif L, Alnæem A, Peiris M (2013) Middle East respiratory syndrome MERS coronavirus seroprevalence in domestic livestock in Saudi Arabia, 2010–2013. Eurosurveillance 18:20659. https://doi.org/10.2807/1560-7917.es.2013.18.50.20659

Holphs D (2014) MERS-CoV enigma deepens as reported cases surge. Lancet 383:1793. https://doi.org/10.1016/s0140-6736(14)60866-7

Horton KC, Wasfy M, Samaha H, Abdel-Rahman B, Safwat S, Abdel-Fadeel M, Mohareb E, Duerger E (2014) Serosurvey for zoonotic viral and bacterial pathogens among slaughtered livestock in Egypt. Vector Borne Zoonotic Dis 14:633–639. https://doi.org/10.1089/vbz.2013.1525

Hunter JC, Nguyen D, Aden B, Al Bandar Z, Al-Dhahi W, Abu Elkeir K, Khudair A, Al Mulla M, El Saleh F, Imambaccus H, Al Kaabi N, Sheikh FA, Sasse J, Turner A, Abdel Wareth L, Weber S, Al Ameri A, Abu Amer W, Alami NN, Bunga S, Haynes LM, Hall J, Kallen AJ, Kuhar D, Pham H, Pringle K, Tong S, Whitaker BL, Gerber SI, Al Hosani FI (2016) Transmission of Middle East respiratory syndrome coronavirus infections in healthcare settings, Abu Dhabi. Emerg Infect Dis 22:647–656. https://doi.org/10.3201/eid2204.151615

Ikegami T, Makino S (2011) The pathogenesis of Rift Valley fever. Viruses 3:493–519. https://doi.org/10.3390/v3030493

IUCN (2008) Camelus ferus: the IUCN red list of threatened species 2008: e. T63543a1268925

Jäckel S, Eiden M, El-Mamy BO, Isselmou K, Vina-Rodriguez A, Sessink M, Grousschup MH (2013) Molecular and serological studies on the Rift Valley fever outbreak in Mauritania in 2010. Transbound Emerg Dis 60:31–39. https://doi.org/10.1111/tbed.12142

Jaros P, Cogger N, French N (2008) A systematic review of the human disease evidence associated with the consumption of raw milk and raw milk cheeses. Massey Univ J Hyg Epidemiol Microbiol Immunol 92:5

Jere KC, Esona MD, Ali YH, Peenzie I, Roy S, Bowen MD, Saed IK, Khalafalla Al, Nyaga MM, Mphahlele J, Steele D, Seher I (2014) Novel NSP1 genotype characterised in an African camel G8P[11] rotavirus strain. Infect Genet Evol 21:58–66. https://doi.org/10.1016/j.meegid.2013.10.002

Jezek Z, Kriz B, Rothbauer V (1983) Camelpox and its risk to the human population. J Hyg Epidemiol Microbiol Immunol 27:29–42

Kaindi DWM, Schelling E, Wangoh JM, Imungi JK, Farah Z, Mele I (2012) Risk factors for symptoms of gastrointestinal illness in Rural Town Isiolo, Kenya: Symptoms of gastroin-
testinal illness in Rural Town Isiolo. *Zoonoses Public Health* 59:118–125. https://doi.org/10.1111/j.1863-2378.2011.01425.x

Kamenetsky L, Gutierrez AM, Canova SG, Haag KL, Guarnera EA, Parra A, Garcia GE, Rosenzvit MC (2002) Several strains of *Echinococcus granulosus* infect livestock and humans in Argentina. *Infect Genet Evol* 2:129–136. https://doi.org/10.1016/S1483-0194(02)00013-4

Karimi M, Ghasemikhah R, Mirahmadi H, Spotin A, Rouhani S, Seyyed Tabaei SJ (2017) Discrimination of mixed infections of echinococcosis species based on in silico sequence analysis: a new way of reflecting overlapping strains in indigenous areas. *Arch Clin Infect Dis* 12:4. https://doi.org/10.3812/archcid.14168

Kayali G, Peiris M (2015) A more detailed picture of the epidemiology of Middle East respiratory syndrome coronavirus. *Lancet Infect Dis* 15:495–497. https://doi.org/10.1016/S1473-3099(15)00128-3

Khalafalla AI, Abdelazim FA (2017) Human and dromedary camel infection with camelpox virus in Eastern Sudan. *Vector Borne Zoonotic Dis* 17:281–284. https://doi.org/10.1089/vbz.2016.2070

Khan AS, Maupin GO, Rollin PE, Noor AM, Shurie HH, Shalabi Khuroo MS, Khuroo MS (2016) Hepatitis E: an emerging global disease. *Emerg Infect Dis* 21:1135–1138. https://doi.org/10.3201/eid2107.150070

Khalafalla AI, Abdelazim F (2017) Human and dromedary camel infection with camelpox virus in Eastern Sudan. *Vector Borne Zoonotic Dis* 17:281–284. https://doi.org/10.1089/vbz.2016.2070

Kleinerman G, Baneth G, Mumcuoglu KY, van Straten M, Berlin J (1997) An outbreak of Crimean-Congo hemorrhagic fever in the United Arab Emirates, 1994–1995. *Trop Med Parasitol* 48:519–525. https://doi.org/10.4269/ajtmh.1997.57.519

Kupferschmidt K (2015) MERS surges again, but pandemic jitters ease. *Science* 347:1296–1297. https://doi.org/10.1126/science.347.6228.1296
from Kenya. J Helminthol 55:21–28. https://doi.org/10.1017/S0022149X00252414

McManus DP, Rishi AK (1989) Genetic heterogeneity within Echinococcus granulosus: isolates from different hosts and geographical areas characterized with DNA probes. Parasitology 99:17–29. https://doi.org/10.1017/S0031182000060984

Megersa B, Biffa D, Abunna F, Regassa A, Godfroid J, Skjerve E (2011) Seroprevalence of brucellosis and its contribution to abortion in cattle, camel, and goat kept under pastoral management in Borana, Ethiopia. Trop Anim Health Prod 43:651–656. https://doi.org/10.1007/s11250-010-9748-2

Megersa B, Biffa D, Abunna F, Regassa A, Godfroid J, Skjerve E (2012) Seroprevalence of ovine and caprine brucellosis in a pastoral region. Epidemiol Infect 140:887–896. https://doi.org/10.1017/S0950268810101178

Memish ZA, Alsahayl A, Masri M, Heil GL, Anderson BD, Peiris M, Khan SU, Gray VC (2015) Rare evidence of MERS-CoV infection among animal workers living in Southern Saudi Arabia during 2012. Influenza Other Respir Viruses 9:64–67. https://doi.org/10.10111/ir.12287

Memish ZA, Baltky HH (2004) Brucellosis and international travel. J Travel Med 11:49–55. https://doi.org/10.1016/S0962-2798(14)70044-1

Memish ZA, Cotten M, Meyer B, Watson SJ, Alsahafi AJ, Memish ZA, Cotten M, Watson SJ, Kellam P, Zumla A, Alhakeem RF, Al-Rabeeah AA, Stephens GM (2014) Community case clusters of Middle East respiratory syndrome coronavirus in Hafr Al-Batin, Kingdom of Saudi Arabia: a descriptive genomic study. Int J Infect Dis 23:63–68. https://doi.org/10.1016/j.ijid.2014.03.1372

Merrill HR, Khan SU, Anderson BD, Heil GL, Alsahly A, Memish ZA, Gray GC, Masri MA (2015) Elevated antibodies against Rift Valley fever virus among humans with exposure to ruminants in Saudi Arabia. Am J Trop Med Hyg 92:739–743. https://doi.org/10.4269/ajtmh.14-0575

Memish ZA, Zumla AI, Al-Hakeem RF, Al-Rabeeah AA, Stephens GM (2013) Family cluster of Middle East respiratory syndrome coronavirus infections. N Engl J Med 368:2487–2494. https://doi.org/10.1056/NEJMoa1303729

Mertens M, Schmidt K, Özkul A, Groschup MH (2013) The impact of Crimean-Congo hemorrhagic fever virus on public health. Antivir Res 98:248–260. https://doi.org/10.1016/j.antiviral.2013.02.007

Meyer B, Juhasz J, Barua R, Das Gupta A, Hakimuddin F, Corman VM, Müller MA, Wernery U, Drosten C, Nagy P (2016) Time course of MERS-CoV infection and immunity in dromedary camels. Emerg Infect Dis 22:2171–2173. https://doi.org/10.3201/eid2212.160832

Meyer B, Müller MA, Corman VM, Reusken CBEM, Ritzi D, Godeke G-J, Lattewie E, Kallies S, Siemens A, van Beek J, Drexler JF, Muth D, Bosch B-J, Wernery U, Koopmans MPG, Wernery R, Drosten C (2014) Antibodies against MERS Coronavirus in dromedary camels, United Arab Emirates, 2003 and 2013. Emerg Infect Dis 20:552–559. https://doi.org/10.3201/eid2004.131746

Miguel E, Chevalier V, Ayele G, Ben Bencheikh MN, Boussini H, Chu DK, El Berbri I, Fassi-Fihri O, Faye B, Fekadu G, Grosbois V, Ng BC, Perera RA, So T, Traore A, Roger F, Peiris M (2017) Risk factors for MERS coronavirus infection in dromedary camels in Burkina Faso, Ethiopia, and Morocco, 2015. Euro-surveillance 22:30498. https://doi.org/10.2807/1560-7917.ES.2017.22.13.30498

Migler E, Perera RAPM, Baubekova A, Chevalier V, Faye B, Akhmetssadykov N, Ng CY, Roger F, Peiris M (2016) Absence of Middle East respiratory syndrome coronavirus in Camelids, Kazakhstan, 2015. Emerg Infect Dis 22:555–557. https://doi.org/10.3201/eid2203.151284

Mirzaei M, Rezaei H, Nematollahi A, Ashrafihelan J (2016) Survey of hydatidosis infection in slaughtered camel CAMELUS DROMEDARIS in Tabriz area, Northwest Iran. J Parasit Dis 40:444–447. https://doi.org/10.1016/s1263-914-0525-6

Moallin ASM, Zessin KH (1988) Outbreak of camel contagious echyma in central Somalia. Trop Anim Health Prod 20:185–186. https://doi.org/10.10107/bf02240991

Mohabbati Mobarez A, Bagheri Amiri F, Esmaeili S (2017) Seroprevalence of Q fever among human and animal in Iran: a systematic review and meta-analysis. PLOS Negl Trop Dis 11:e0005521. https://doi.org/10.1371/journal.pntd.0005521

Mohedi I, Madadi H, Arfaa F (1970) Camel, CAMELUS DROMEDARISAS, as intermediate host of Echinococcus granulosus in Iran. J Parasitol 56:1255. https://doi.org/10.2307/2377581

Moda G, Daborn CJ, Grange JM, Cosivi O (1996) The zoonotic importance of Mycobacterium bovis. Tuberc Lung Dis 77:103–108. https://doi.org/10.1016/S0962-8479690022-2

Mohd HA, Al-Tawfiq JA, Memish ZA (2016) Middle East respiratory syndrome coronavirus MERS-CoV origin and animal reservoir. Virol J 13:87. https://doi.org/10.1186/s12985-016-0544-0

M’rad S, Filisetti D, Oudni M, Mekki M, Belghiti M, Nouri A, Sayadi T, Lahmar S, Candolfi E, Azaiez R, Mezhoud H, Babha H (2005) Molecular evidence of ovine G1 and camel G6 strains of Echinococcus granulosus in Tunisia and putative role of cattle in human contamination. Vet Parasitol 129:267–272. https://doi.org/10.1016/j.vetpar.2005.02.006

Muhairi SA, Hosani FA, Eltahir YM, Mulla MA, Yusof MF, Serhan WS, Hashem FM, Elsayed EA, Marzoug BA, Abdelazim AS (2016) Epidemiological investigation of Middle East respiratory syndrome coronavirus in dromedary camel farms linked with human infection in Abu Dhabi Emirate, United Arab Emirates. Viruses Genes 52:848–854. https://doi.org/10.1186/s12262-016-1367-1

Muloi D, Alarcon P, Ombui J, Ngeiywa KJ, Abdullahi B, Muinde P, Karani MK, Rushton J, Fevre EM (2018) Value chain analysis of camel milk production and animal health. J Prev Med 59:203–210. https://doi.org/10.1016/j.jprevmed.2018.09.010

Müller MA, Corman VM, Jores J, Meyer B, Younan M, Liljander A, Bosch B-J, Lattewie E, Hilali M, Musa BE, Bornstein S, Drosten C (2014) MERS coronavirus neutralizing antibodies in camels, Eastern Africa, 1983–1997. Emerg Infect Dis 20:2093–2095. https://doi.org/10.3201/eid2012.141026

Müller MA, Meyer B, Corman VM, Al-Masri M, Turkestan A, Ritzi D, Sieberg A, Aldabbagh S, Bosch B-J, Lattewie E, Alha-keem RF, Assiri AM, Albarrak AM, Al-Shangiti AM, Al-Tawfiq JA, Wikramaratna P, Alrabeeah AA, Drosten C, Memish ZA (2015) Presence of Middle East respiratory syndrome coronavirus antibodies in Saudi Arabia: a nationwide, cross-sectional, serological study. Lancet Infect Dis 15:559–564. https://doi.org/10.1016/S1473-30991570090-3
Rasmussen SA, Gerber SL, Swerdlow DL (2015) Middle East respiratory syndrome coronavirus: update for clinicians. *Clin Infect Dis* 60:1686–1689. https://doi.org/10.1093/cid/civ118

Rasmussen SA, Watson AK, Swerdlow DL (2016) Middle East respiratory syndrome MERS. *Microbiol Spectr* 4:3. https://doi.org/10.1128/microbiolspec.EI0-0020-2016

Raufu IA, Odetokun IA, Oladunni FS, Adam M, Kolapo UT, Rasmussen SA, Watson AK, Swerdlow DL (2016) Co-circulation of three camel coronavirus species and recombination of MERS-CoVs in Saudi Arabia. *Science* 351:81–84. https://doi.org/10.1126/science.aac8608

Roser M (2018) Future population growth. *Our world in data*. https://ourworldindata.org/future-population-growth. Accessed May 3, 2018

Sahib JSM, Lam TT-Y, Ahmed MMM, Li L, Shen Y, Abo-Abba S, Qureshi MI, Abu-Zeid M, Zhang Y, Khiyami MA, Alhbari NS, Hajrah NH, Sabir MJ, Mutwakil MHZ, Kabli SA, Alsulfaimany FAS, Obaid AY, Zhou B, Smith DK, Holmes EC, Zhu H, Guan Y (2016) Co-circulation of three camel coronavirus species and recombination of MERS-CoVs in Saudi Arabia. *Science* 351:81–84. https://doi.org/10.1126/science.aac8608
Seleem MN, Boyle SM, Sriranganathan N (2010) Brucellosis: a re-emerging zoonosis. Vet Microbiol 140:392–398. https://doi.org/10.1016/j.vetmic.2009.06.021

Shaalan MA, Memish ZA, Mahmoud SA, Alomari A, Khan MY, Almuneef M, Alalota S (2002) Brucellosis in children: clinical observations in 115 cases. Int J Infect Dis 6:182–186. https://doi.org/10.1016/S1201-9712(02)90108-6

Shahana II, Zaraket H, Suzuki H (2013) Molecular studies on diarrhea-associated Escherichia coli isolated from humans and animals in Egypt. Vet Microbiol 167:532–539. https://doi.org/10.1016/j.vetmic.2013.08.014

Shah Nazi M, Hejazi H, Salehi M, Andalib AR (2011) Molecular characterization of human and animal Echinococcus granulosus isolates in Isfahan, Iran. Acta Tropica 117:47–50. https://doi.org/10.1016/j.actatropica.2010.09.002

Shakerian A, Shekarforoush SS, Ghafari Rad H (2008) Prevalence of Linguatula serrata nymphs in one-humped camel Camelus dromedarius in Najaf-Abad, Iran. Res Vet Sci 84:243–245. https://doi.org/10.1016/j.resvetsci.2007.04.015

Shapiro M, London B, Nigri D, Shoss A, Zilber E, Fogel I (2016) Middle East respiratory syndrome coronavirus: review of the current situation in the disaster. Mil Med 29: https://doi.org/10.1186/s13071-015-1025-9

Shariatzaadeh SA, Spotin A, Gholami S, Fallah E, Hazrati A, Mahami-Oskouei M, Montazeri F, Moslemzadeh HR, Shahbazi A (2015) The first morphometric and phylogenetic perspective on molecular epidemiology of Echinococcus granulosus sensu lato in stray dogs in a hyperendemic Middle East Focus, northwestern Iran. Parasites Vectors 8:409. https://doi.org/10.1186/s13071-015-1025-9

Sharif-Yakan A, Kanj SS (2014) Emergence of MERS-CoV in the Middle East: Origins, Transmission, Treatment, and Perspectives. PLoS Pathog 10:e1004457. https://doi.org/10.1371/journal.ppat.1004457

Sharma SK, Kataria AK, Shringi BN, Nathawat P, Bhati T, Mohammed N (2013) Detection of hypermucoviscos Klebsiella pneumoniae in camel Camelus dromedarius during an outbreak of acute respiratory tract infection. J Camel Pract Res 20:139–143

Sharma M, Sehgal R, Fomda BA, Malhotra A, Malla N (2013) Molecular characterization of Echinococcus granulosus cysts in North Indian patients: identification of G1, G3, G5 and G6 genotypes. PLoS Negl Trop Dis 7:e2262. https://doi.org/10.1371/journal.pntd.0002262

Shchelkunov SN (2013) An increasing danger of zoonotic or-fthropoxvirus infections. PLoS Pathog 9:e1003756. https://doi.org/10.1371/journal.ppat.1003756

Shenfeld KM, Gomaa MR, Ali MA, Kayali G (2016) Middle East respiratory syndrome coronavirus: a comprehensive review. Front Med 10:120–136. https://doi.org/10.3389/fmed.2016.016430-6

Shinol SB, Dukhan L, Belmaker I, Bardenstein S, Sibirsky D, Barrett C, Greenberg D (2012) Human brucellosis outbreak acquired through camel milk ingestion in southern Israel. Israel Med Assoc J 14:475–478

Singh BB, Dhand NK, Ghatak S, Gill JPS (2014) Economic losses due to cystic echinococcosis in India: need for urgent action to control the disease. Prev Vet Med 113:1–12. https://doi.org/10.1016/j.prevetmed.2013.09.007

Smits HL, Kadri SM (2005) Brucellosis in India: a deceptive infectious disease. Indian J Med Res 122:375–384

Spahr C, Knauf-Witzen S, Vahlenkamp T, Ulrich RG, Johnen R (2018) Hepatitis E virus and related viruses in wild, domestic and zoo animals: a review. Zoonoses Public Health 65:11–29. https://doi.org/10.1111/zph.12405

Spotin A, Gholami S, Najafi Nasab A, Fallah E, Oskouei MM, Semnani V, Shariatzaadeh SA, Shahbazi A (2015) Designing and conducting in silico analysis for identifying of Echinococcus spp. with discrimination of novel haplotypes: an approach to better understanding of parasite taxonomy. Parasitol Res 114:1503–1509. https://doi.org/10.1007/s00436-015-4334-1

Spotin A, Mahami-Oskouei M, Harandi MF, Baratchian M, Bordbar A, Ahmadpour E, Ebrahimisima S (2017) Genetic variability of Echinococcus granulosus complex in various geographical populations of Iran inferred by mitochondrial DNA sequences. Acta Trop 165:10–16. https://doi.org/10.1016/j.actatropica.2016.03.002

Sprague LD, Al-Dahouk S, Neubauer H (2012) A review on camel brucellosis: a zoonosis sustained by ignorance and indifference. Pathog Glob Health 106:144–149. https://doi.org/10.1179/2047773212Y.0000000020

Stenseth NC, Atshabar BB, Begon M, Belmain SR, Bertherat E, Carniel E, Gage KL, Leirs H, Rahalison L (2008) Plague: past, present, and future. PLoS Medicine 5:e3. https://doi.org/10.1371/journal.pmed.0050003

Su S, Wong G, Shi W, Liu J, Lai ACK, Zhou J, Liu W, Bi Y, Gao GF (2016) Epidemiology, genetic recombination, and pathogenesis of coronaviruses. Trends Microbiol 24:490–502. https://doi.org/10.1016/j.tim.2016.03.003

Sung JM-L, Lloyd DH, Lindsay JA (2008) Staphylococcus aureus host specificity: comparative genomics of human versus animal isolates by multi-strain microarray. Microbiology 154:1949–1959. https://doi.org/10.1099/mic.0.2007/015289-0

Swai ES, Sindato C (2015) Seroprevalence of Rift Valley fever virus infection in camels dromedaries in northern Tanzania. Trop Anim Health Prod 47:347–352. https://doi.org/10.1007/s12250-014-0726-y

Tadesse G (2015) A meta-analysis of the proportion of animal Salmonella isolates resistant to drugs used against human salmonellosis in Ethiopia. BMC Infect Dis 15:84. https://doi.org/10.1186/s12879-015-0835-x

Tai W, Wang Y, Fett CA, Zhao G, Li F, Perlman S, Jiang S, Zhou Y, Du L (2017) Recombinant Receptor-binding domains of multiple Middle East respiratory syndrome coronaviruses MERS-CoVs induce cross-neutralizing antibodies against divergent human and camel MERS-CoVs and antibody escape mutants. J Virol 91:e01651-16. https://doi.org/10.1128/JVI.01651-16

Tejedor-Junco MT, González-Martín M, Noé Francisco RG (2015) Identification, antimicrobial susceptibility, and virulence factors of Enterococcus spp. strains isolated from Camels in Canary Islands, Spain. Vet Ital 5:179–183. https://doi.org/10.12834/vetit.322.1280.2

Teshome H, Molla B, Tibbo M (2003) A seroprevalence study of camel brucellosis in three camel-rearing regions of Ethiopia. Trop Anim Health Prod 35:381–390. https://doi.org/10.1023/A:1025874310261

Tigre D, Ferreira D, Haile A, Gabriel S, Victor B, Pelt JV, Devleeschauwer B, Vercruysse J, Dormy P (2016) Molecular characterization of Echinococcus granulosus s.l. cysts from cattle, camels, goats and pigs in Ethiopia. Vet Parasitol 215:17–21. https://doi.org/10.1016/j.vetpar.2015.10.022

Teshome H, Molla B, Tibbo M (2003) A seroprevalence study of camel brucellosis in three camel-rearing regions of Ethiopia. Trop Anim Health Prod 35:381–390. https://doi.org/10.1023/A:1025874310261

Tigre D, Ferreira D, Haile A, Gabriel S, Victor B, Pelt JV, Devleeschauwer B, Vercruysse J, Dormy P (2016) Molecular characterization of Echinococcus granulosus s.l. cysts from cattle, camels, goats and pigs in Ethiopia. Vet Parasitol 215:17–21. https://doi.org/10.1016/j.vetpar.2015.10.022
