Main risk factors associated with small and large ruminant brucellosis

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Abstract:

Brucellosis is a neglected zoonotic bacterial disease in most of the developing world that has a significant impact on public health. The prevalence of brucellosis in livestock, particularly in large and small ruminants is variable in many countries and seems to remain high, especially amongst subsistence and small-scale livestock farmers. There are different factors that may influence the prevalence of brucellosis in large and small ruminants. This review is aiming at describing the most important factors that need to be taken into consideration for the planning and implementation of effective brucellosis control programmes . Common risk factors in the brucellosis development in small and large ruminant animals include species, age, sex, extensive or intensive production system, herd/flock size, mixed farming, introduction of new animals in the farms, breeding practice, hygiene, absence of vaccination, and awareness of the disease. This review suggests that different risk factors might have various impact on brucellosis seroprevalence that need to be addressed in epidemiological studies in different farming systems,

Keywords: Brucellosis, risk factor, small ruminant, large ruminant

Introduction

According to the World Health Organization (WHO), the Office International des Epizooties (OIE), and the Food and Agriculture Organization (FAO), brucellosis is still one of the most widespread and important zoonotic infection in developing countries (B Lopes et al. 2010; Seleem et al. 2010). This disease is a source of different economic concerns because of infertility in both sexes and late term abortion (Angara et al. 2016; Awah-Ndukum et al. 2018; Deka et al. 2018; Franc et al. 2018; Sulima and Venkataraman 2010), decreased milk yield (Herrera et al. 2008; Mellado et al. 2014) loss of draught power and market value of animals, missed reproductive cycle, decreased productivity, increased veterinary costs, and birth of weak offspring with low birth weight in farms (Blasco and Molina-Flores 2011; Dadar et al. 2020; Lokamar et al. 2020). Brucellosis is a chronic and infectious zoonotic disease of domestic and wild animals caused by several species of *Brucella* bacteria (Franc et al. 2018). Currently, twelve species could infect different domestic and wild animal species

(Whatmore et al. 2016). Among them, six *Brucella* species have been divided based on their preferred hosts and pathogenicity as *Brucella melitensis* (goats and sheep), *Brucella abortus* (cattle), *Brucella suis* (pigs), *Brucella ovis* (rams), *Brucella canis* (dogs), and *Brucella neotomae* (desert wood rat, common voles). *B. melitensis, B. suis,* and *B. abortus* are known as the most important pathogenic species in livestock (Dadar et al. 2019a; Kaynak-Onurdag et al. 2016; Lindahl et al. 2014; Omer et al. 2000; Wareth et al. 2014; Whatmore et al. 2016), while *Brucella. melitensis* is the main source of human infections (Dadar et al. 2019b; Dadar et al. 2019c). Beside well-known endemic regions located in Africa, South and Central America, the Mediterranean Basin, Middle East, and Asia, brucellosis remains a neglected disease in several areas which can lead to serious economic concern for the livestock industry (Bamaiyi 2015; Mableson et al. 2014; Santos et al. 2013; Singh et al. 2015; Sulima and Venkataraman 2010). The aim of this mini-review was to highlight potential risk factors for *Brucella* infections in small and large ruminants.

Brucellosis in large ruminants

Brucella abortus has been known as a Gram-negative coccobacillus bacteria in the class Alphaproteobacteria, family Brucellaceae that commonly infects cattle and other bovinae as the primarily hosts. *Brucella abortus* is divided into eight biovars (1-7, 9), of which biovars 1 to 3 are the most commonly isolated biovars from humans. *Brucella melitensis*, *B. canis* and *B. suis* have been reported as other *Brucella* species that could be isolated in cattle (Khurana et al. 2021). Reservoir hosts of *B. abortus* are reported as cattle, water buffalo, African buffalo, American bison (*Bison bison*), and elk (*Cervus elaphus nelsonii*) (Abubakar et al. 2012; Dadar et al. 2019a; Dadar et al. 2021). However, other species such as sheep, pigs, camel and horse might also sustain *B. abortus* for a certain period of time (Alamian and Dadar 2019; Fiebig et al. 2021), although such infection is almost always reported to be associated to the presence of infected animal in reservoir species (Godfroid, 2013). It has been reported that a number of countries like European Union Member States, New Zealand, Australia, Canada, the USA Israel, and Japan eliminated bovine brucellosis through eradication programs (Abubakar et al. 2012), although *B. abortus* infection is still found worldwide in bovinae of Asia, South and Central America, Africa, the Mediterranean Basin, Sahara and the Caribbean (Corbel 1997). Wildlife reservoirs of *B. abortus* are elk and bison in parts of North America (Olsen 2010). The infection of cattle by *B. abortus* occurs by close contact to birth products, including fetus, fetal fluids placenta, and vaginal discharges of infected animals. Moreover, the bacteria can also enter the body of animal through lesions in the skin. Cattle can shed *B. abortus* whether they carry the pregnancy to term or abort and remain infected for years. *Brucella abortus* is also shed in semen, milk and urine (Aune et al. 2012; Capparelli et al. 2009). Vaccination of cattle can help to decrease the *B. abortus* prevalence during control programs and the clinical signs of brucellosis in infected herds (Cheville et al. 1996; Yang et al. 2013). Generally, two licensed live attenuated vaccines are used for *B. abortus* infection in cattle, including *B. abortus* strain 19 (S19), and *B. abortus* RB51, although other vaccines such as the S2 *B. suis* vaccine in China, and the strain 75/79-AB and 82 *B. abortus* vaccines in Russia are used (Yang et al. 2013). Importantly, these later vaccines are not recommeneded by the OIE (https://www.oie.int). The performance of these animal vaccines is dependent upon the host species, route, and dose of immunization (de Oliveira et al, 2021).

Brucellosis in small ruminants

Brucella melitensis is describe as a Gram negative coccobacillus in the class Alphaproteobacteria and family Brucellaceae that mainly infects sheep and goats as reservoir hosts. *B. melitensis* is divided into three biovars (that are actually only serovars). *Brucella suis* and *B. abortus* have been reported occasionally as other *Brucella* species in small ruminants, although there are rare clinical symptoms caused by these species (Gumaa et al. 2014; Wareth et al. 2015). Infection with *B. melitensis* also have also been described in cattle, water buffalo, yaks (*Bos grunniens*), dromedary and Bactrian camels, pigs, alpacas, horses and dogs (Alamian and Dadar 2020; Dadar and Alamian 2020). Wildlife reservoirs of *B.melitensis* is reported as Iberian wild goats (*C. pyrenaica*), chamois (*Rupicapra rupicapra*), wild Alpine ibex (*Capra ibex*), sable antelope (*Hippotragus niger*), impala (*Aepyceros melampus*), bharal goats (*Pseudois nayaur*) and Arabian oryx (*Oryx leucoryx*). Infection by *B. melitensis* has been reported in the most Mediterranean countries, the Middle East, some southern and eastern European countries, South-West of Asia and parts of Latin America and Africa (Erganis et al. 2005; Janowicz et al. 2020). The most common routes of *B. melitensis* infection in small ruminants is close contact with birth products such as fetus, placenta, fetal fluids and vaginal discharges of infected animals. The infection in sheep and goats may persistfor years (Tittarelli). Small ruminant animals can shed *B. melitensis* in the vaginal discharges, semen, urine and milk. Currently, the control of small ruminant brucellosis has been performed through the licensed live attenuated vaccine of *B. melitensis* Rev. 1 (Banai 2002).

Potential risk factors associated with small ruminant brucellosis

The most significant factors in the brucellosis persistence in many regions of world need extensive and in depth analysis of associated risk factors (B Lopes et al. 2010; Moosazadeh et al. 2016; Ning et al. 2013). Brucellosis is considered as an occupational threat for subsistence, small-scale goat and sheep farmers and pastoralists because of the lack of awareness regarding quarantine practices as well as specific safety recommendation for brucellosis and absence of knowledge of transmission routes to humans (Peck et al. 2019). Furthermore, the consumption of raw dairy products is another important risk factor due to the common shedding of *Brucella* spp. (specially *B. melitensis*) into the milk of infected livestock (Dadar et al. 2019c). Risk factors for brucellosis seroprevalence in sheep and goat flocks were reported asbreed, contact with other animals (cattle, horse, monkey, dog, cat), herd size with more animal's movements and intensive management practices, age at animal population level, the incorporation on new animals to the flock during the previous year, frequency of disinfecting practices per year, implementation of brucellosis control programs for sheep and goat flocks, type of grazing, feeding, mate control, origin of the farm (Kelkay et al. 2017; Lindahl et al. 2014; Saleem 2019; Teklue et al. 2013). Abortion history in small-ruminant was a significant risk factor with flock-level seropositivity of brucellosis (Abnaroodheleh et al. 2021; Megersa et al. 2011). Brucellosis seropostiveity was also reported as significantly associated with history of retained fetal membrane in small ruminants (Adem et al. 2021).

Species, age, and sex of the small ruminants also were reported to influence the occurrence of brucellosis among flocks (Behera et al. 2020; Dabassa et al. 2013). Furthermore, it has been showed that lack of corral hygiene, large flock size, high animal density, uncontrolled animal movements, close contact between sheep and goats, shared pasture for grazing, and mixed herding with large ruminants are important risk factors for *Brucella* infection (Primatika et al. 2016; Teklue et al. 2013). A case–control study with 255 small ruminants herds and multivariable logistic regression model in Portugal demonstrated that the lake of cleaned watering places, contamination of the water with urine and faeces, insufficient cleaning premises and insufficient manure removal, introduction of animals from herds of unknown status or from infected brucellosis herds and the herds with more than 116 animals are important as risk factors for *Brucella* seropositivity (Coelho et al. 2007). Moreover, the univariable logistic regression analysis on individual animal-level risk factors was showed altitude/agro-ecology as one of the flock-level risk factors considered during the brucellosis evaluation in small ruminants in Ethiopia. This analysis reported higher seroprevalence in the mid-highland (30.8 %) and lowland (50 %) in compared with highland (5 %)(Teklue et al. 2013).

Potential risk factors associated with large ruminant brucellosis

The prevalence of large ruminant brucellosis is related to herd size (Terefe et al. 2017) . Herd size is a critical risk factor due to the contact among and within herds, and the impact of environmental and management factors related to herd size (Cowie et al. 2014; Mai et al. 2013; Matope et al. 2010). It has been also reported that seropositivity was significantly related to the calves number per cow (ref?). In addition, a number of possible risk factors for *Brucella* seropositivity in dairy cattle farms have been reported asincreasing stocking density, the presence of other animal species (horses, dog, monkey, sheep, goat, cat, poultry) in the farm, purchase source and frequency, the type of service used for breeding (artificial or natural insemination), type of personnel used (hired or family members), methods of disposal of manure, use of calving pens, and use of permanent housing for cows (Omer et al. 2000). Using a negative binomial regression model, the seropositivity of cattle appeared to be independently related to geographical area, stocking density, keeping mixed breed herds, and herd size (Matope et al. 2010). However, no association between brucellosis prevalence and geographical locations was observed in farms that were located in the mountainous areas, plain and hilly areas, and the large herds far from main roads of Tanzania (Ukita et al. 2021). Furthermore, the cattle breed management and the lack of knowledge about brucellosis by farmers were independently related to the rate of abortion in small household herds from different areas of Zimbabwe (Matope et al. 2010; Pathak et al. 2016). The poor implementation of brucellosis control programs for livestock, including testing of animals, reporting disease to the veterinary services and movement of infected cattle were reported as important risk factors for bovine brucellosis (Awah-Ndukum et al. 2018; Pathak et al. 2016). Recently epidemiological investigations reported that the breed of dairy cattle, abortion history and abortion period along with farm location had important effect on the brucellosis incidence among dairy cattle (Akinseye et al. 2016; Carbonero et al. 2018; Geresu et al. 2016; Halliday et al. 2015). A cross sectional study showed that the seroprevalence of bovine is significantly associated with various risk factors including the reproductive status, number of service per conception, age, gender, and calving interval (Asgedom et al. 2016). Sharing water sources for cattle within and outside farms as well as having a history of reactor cattle for brucellosis are significant risk factors for *Brucella* infection in dairy cattle farms (Tukana and Gummow 2017). The important risk factor for high prevalence of cattle brucellosis in endemic areas of Tanzania was determined as the introduction of cattle from other herds (Ukita et al. 2021).

Potential risk factors related to brucellosis in camel due to either *B. melitens*is or *B. abortus,* were evaluated using a multivariable logistic regression model in several studies and a significant association was reported with the lack of adequate *Brucella* control program in cattle, and sheep and goat, contact with other livestock species, particularly ruminants, uncontrolled animal transportation, absence of hygienic measures (Al-Majali et al. 2008; Alamian and Dadar 2019; Fatima et al. 2016), locality, herd size and contact with other camels (Ghanem et al. 2009), season, abortion, and orchitis history (Fatima et al. 2016).

Conclusion

The main risk factors reported in this review support current recommendations for brucellosis control. Brucellosis is a neglected zoonotic disease with serious consequences on the reproductively and productivity of small and large ruminants. It is thus important to improve both preventive and control methods through the evaluation of potential risk factors impacting livestock health and economy. The spread of *Brucella* infection has been affected by the type of husbandry system implemented and the presence of abortion in small and large ruminant was the most important risk factors for brucellosis seropositivity. However, the type of animal species has a statistically significant effect on seroprevalence. The common flock/herd-level risk factors evaluated during different studies were flock/herd size, common grazing lands, purchase of animal with unknown brucellosis status, abortion management, altitude/agro-ecology, sharing of breeding ram/buck/bulls, keeping of animals together, and dog presence (scavenging aborted materials). Moreover, the poor farmers' awareness and perception on abortion management and brucellosis transmission could aggravate the situation of disease on the farm.

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