

K-27**Zoonotic risks from small ruminants**

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E-mail: benjamin.bauer@tiho-hannover.de**Keywords:** Emerging infectious diseases; Interdisciplinary collaborations; Public Health; Surveillance

In accordance with the WHO, “A zoonosis is an infectious disease that has jumped from a non-human animal to humans”. Zoonotic pathogens may be bacterial, viral, parasitic, or fungal. The pathogens can spread to humans through direct contact, inhalation, food and water or transmitted by vectors. Zoonoses cause major public health problems around the world due to the close relationship between humans and livestock, companion animals and with wildlife.

The awareness of zoonotic pathogens in small ruminants has increased in recent years. In Europe different zoonotic diseases (re-)emerged in the last two decades. In the Netherlands, *Coxiella burnetii* infected dairy goats caused the world-wide largest human Q fever outbreak from 2007 to 2012. Tremendous efforts have been undertaken to control the disease on goat farms. Moreover, intensive research purposes contributed to a better understanding of *C. burnetii*. In other European countries, human Q fever cases are associated with lambing sheep. New research showed that year-round lambing increases the risk of *C. burnetii* in sheep flocks. Vaccination of female offspring before mating seems to be an effective and cost-efficient way to prevent *C. burnetii* outbreaks in sheep flocks.

Due to the increasing popularity of drinking raw milk, and new marketing channels for raw milk through vending machines and internet sale, it is necessary to raise the awareness of food-borne pathogens in raw milk (products). Apart from the classic foodborne pathogens such as thermophilic *Campylobacter*, other pathogens are less in focus. For instance, the Tick-borne Encephalitis Virus (TBEV) is also transmitted to humans through the consumption of raw goat milk (products), as has been reported from several countries such as Germany, Slovakia and Croatia. The virus is transmitted by infected ticks to goats, and they are shedding the pathogen with milk up to 23 days post infection. Therefore, milk pasteurization is strongly recommended.

New zoonotic potential of neglected pathogens has been identified with advanced molecular techniques. For example, the classical Borna Disease Virus (BDV) is not transmitted from infected sheep to humans to the current knowledge. The bicolored shrew is supposed to be the reservoir of BDV and the pathogen is transmitted by their excretion to humans, sheep and other susceptible species.

Despite the risk of pathogen spillovers from small ruminants to humans, especially sheep offer the opportunity to act as sentinels to identify the emerge of zoonotic diseases such as TBEV, Rift Valley Fever Virus and Crimean-Congo Hemorrhagic Fever Virus. An interdisciplinary approach is urgently needed to prevent transmission. Close collaborations between human and veterinary medicine and scientists from other fields such as ecologists and meteorologists are desirable. Linking data of passive and active surveillance systems from both disciplines will increase the preparedness for future disease outbreaks.

doi: [10.1016/j.anscip.2023.01.037](https://doi.org/10.1016/j.anscip.2023.01.037)**K-28****Control of sheep and goat brucellosis**

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Brucellosis is a zoonosis caused by *Brucella*, a genus of gram-negative bacteria that behave as facultative intracellular pathogens of ruminants, suidae, canids, camelids, marine mammals and wildlife. *Brucella* causes reproductive failure in livestock and undulant fever (among other symptoms) in humans. Worldwide, sheep and goat brucellosis caused by *B. melitensis* is the greatest threat for humans and controlling the infection in livestock does not only improves animal production but it's the most effective and practical way to prevent human contagion.

Eradication of *B. melitensis* has been achieved in several European Union (EU) countries after many years of effort and heavy investment in official campaigns. However, the infection remains prevalent in some regions of the EU and in most resource-limited countries all over the world. The attenuated live *B. melitensis* Rev1 vaccine (the only vaccine available for sheep and goat brucellosis) has been instrumental for the control and eradication of *B. melitensis*. However, Rev 1 causes abortions when administered to pregnant females and may interfere in the serological tests used routinely for *B. melitensis* surveillance. Wherever *B. melitensis* has been eradicated, these drawbacks have been overcome by limiting vaccination to young replacement animals by the conjunctival route, and by applying a combined test-and-slaughter policy. This strategy requires individual identification, strict control of animal movements and a generous budget for logistics and compensation for culling. These requisites are unfeasible in resource-limited areas, where mass vaccination of both young and adult animals (including those pregnant) becomes necessary. In these situations, the vaccine serological interference is irrelevant because culling cannot be

implemented, but the abortifacient effect of Rev 1 is a serious issue when vaccinating pregnant animals. Indeed, to develop a safe *B. melitensis* vaccine providing a good protection but lacking the abortifacient effects is currently the main goal of brucellosis vaccine research. Although non-zoonotic, *B. ovis* (which affect sheep exclusively) also poses a significant problem as a widespread cause of infertility in rams and abortions or perinatal mortality in sheep. Rev 1 vaccine is also effective against *B. ovis* but due to its safety issues and potential diagnostic interferences, this vaccine is banned in those regions where *B. melitensis* eradication has been achieved. Consequently, *B. ovis* is re-emerging in *B. melitensis* free areas, and causes a grave problem in sheep in those countries where Rev 1 vaccination has been never implemented. Specific surveillance and control programs need to be implemented to avoid the spread of *B. ovis* in these areas. Thus, the development of *B. ovis* specific vaccines not interfering in *B. melitensis* surveillance is worth to be investigated.

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Q fever in a future pan-European surveillance perspective

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Q fever is an almost ubiquitous zoonosis caused by *Coxiella burnetii*, which is able to infect several animal species, as well as humans. Cattle, sheep and goats are the primary animal reservoirs. In small ruminants, infections are mostly without clinical symptoms, however, abortions and stillbirths can occur, mainly during late pregnancy. Shedding of *C. burnetii* occurs in faeces, milk and, mostly, in placental membranes and birth fluids. During parturition of infected small ruminants, bacteria from birth products become aerosolised. Transmission to humans mainly happens through inhalation of contaminated aerosols. In the last decades, there have been several, sometimes large, human Q fever outbreaks related to sheep and goats, and often originated from a single farm or a single event. At the end of the first decade in this century, the largest recorded outbreak occurred in the Netherlands, with over 4,000 patients, and was related to *C. burnetii* shedding dairy goats. In order to prevent human Q fever outbreaks, several measures were implemented in the Netherlands. Of the implemented measures, mandatory vaccination with inactivated phase I vaccine (Coxevac[®], CEVA Santé Animale) has played an important role in the reduction of bacterial shedding. Development of alternative Q fever vaccines has been rather limited, recent advances in methods to identify candidate vaccine antigens have shown considerable promise for the development of next-generation subunit vaccines, and will be discussed in this presentation.

An important role in source tracing can be played by genotyping of the bacterium. Whole genome sequencing (WGS) has revolutionised molecular epidemiology and surveillance of many zoonotic pathogens as it provides comprehensive genetic information and is easily standardised. Recently, a pan-European consortium has been proposed with the aim of collating *C. burnetii* positive samples from a wide range of hosts like livestock, wildlife and humans, with accurate clinical data. Isolated strains, plus available archived strains, will be submitted for WGS to generate a comprehensive database of annotated *C. burnetii* genomes, and phenotypic data from the field and *in-vitro* cellular assays as proxies of *in vivo* virulence. WGS data will be analysed using novel bioinformatics approaches to identify molecular determinants of *C. burnetii* host range and virulence. An important aim of this project is to create a pan-European framework for future molecular surveillance of *C. burnetii*. These opportunities in surveillance and advanced techniques will most likely bring source tracing of *C. burnetii* infections to a next level.

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Bluetongue

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Bluetongue (BT) is a non-contagious, viral disease affecting domestic and wild ruminants (primarily sheep and including cattle, goats, buffalo, antelope, deer or elk) that is transmitted by midges of the *Culicoides* species.

The virus which causes BT is identified as a member of Orbivirus genus of the family Reoviridae. The BT virus species, or serogroup, contains 24 notifiable serotypes, and some other atypical serotypes recently described. Infection with bluetongue virus (BTV) can occur asymptotically in many animals, but can cause fatal disease in a proportion of infected ruminants. The severity of disease varies among