The Dutch Q Fever Situation - Lessons Learned?¹

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Abstract – About 60 to 75% of the emerging infectious diseases are zoonotic. A special group of zoonotic diseases are those that are endemic but in a dormant state. A good example of such a disease is Q fever in the Netherlands. Before 2005, Q fever was known to be present in the human and animal populations but did not cause significant disease. This changed in 2005, when the first abortions in dairy goats were registered and in 2007 when the first human Q fever outbreak in the Netherlands was recorded. Between 2005 and 2009 abortions on 28 dairy goat farms and 2 dairy sheep farms were detected and between 2007 and 2010 about 4000 human cases were notified. This is recognised as the largest laboratory confirmed Q fever outbreak ever reported. To identify the cause of the human disease, genotyping of the causative Q fever agent Coxiella burnetii confirmed the epidemiological link between humans and dairy goats and sheep. Furthermore, an intergraded human-veterinary approach was needed to combat the outbreak. The need for such a One Health approach was also the conclusion of the official evaluation of the Q fever outbreak in the Netherlands. This resulted in a currently implemented national zoonosis structure with a signalling forum that meets monthly. This structure has already been helpful in assessing the human risk of the Schmallenberg virus outbreak.

Keywords – Q fever, zoonosis, outbreak response, signalling

1. Introduction

About 60 to 75% of emerging infectious diseases are zoonotic. These diseases with animals as a reservoir can cause significant disease burden in the human population, depending on the disease, prevalence and transmission routes. To assess the risk of zoonotic diseases, knowledge from veterinary as well as from human medicine is needed. This is particularly true in the case of outbreak management, where good cooperation between the human and veterinary fields is needed and this has to be supported with up to date data and tools.

A special group of zoonotic diseases are those that are already endemic but with a known lack of knowledge about prevalence, host species and genotypes in humans and animals. Normally, the dormant endemic situation is present for years and attracts little attention. A recent example of this is the unprecedented Q fever outbreak in the Netherlands. At the start of the Q fever epidemic (in 2005 in dairy goats and in 2007 in humans) prevalence, host species and genotypes were unknown and structures and tools to exchange knowledge between the human and veterinary domains were lacking. This hugely hampered outbreak management at the start of the Q fever epidemic. Since the evaluation of the Q fever outbreak, structures to facilitate the cooperation between the human and veterinary fields have been implemented.

This paper provides an overview of the Dutch Q fever outbreak and the lessons learned which resulted in an integrated human-veterinary risk analysis structure.

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2. The Dutch fever situation

2.1. Summary of the outbreak

Since the 1950s, Q fever has been present in the Netherlands, but only a few human cases were reported until the 1970s. In 1975, Q fever became notifiable for humans (van Vliet, 2009) and since that time an average of about 20 cases has been reported each year. The first human outbreak of Q fever in the Netherlands was reported in 2007: 168 cases were registered in the south of the Netherlands. In 2008 and 2009, the annual number of human cases increased to 1000 and 2355 respectively. Over the years 2007-2010, 4000 human cases were reported making the Dutch Q fever outbreak the largest laboratory confirmed Q fever outbreaks ever seen.

Until 2005, serological investigations confirmed the presence of Q fever in the animal population although no clinical symptoms were described. This changed in 2005. Slightly ahead of the human outbreak, Q fever problems started in the dairy goat and dairy sheep populations with abortion rates of up to 80 % per herd (Wouda and Derksen, 2007). Between 2005 and 2009 a very large number of abortions were registered on 28 dairy goat farms and 2 dairy sheep farms. With goat numbers of between 600 and 7000 per herd, huge quantities of Coxiella burnetii (the Q fever bacterium) were spread in the environment during abortion and early birth. These bacteria were transported to the neighbouring human population by the prevailing north-east winds in pre-dry spring periods. All of this happened in the south-eastern part of the Netherlands, which is highly populated and has a dense dairy goat infrastructure (Roest et al., 2011b). Eventually, the connection between dairy goats and humans was primary based on epidemiological findings. This connection was confirmed by preliminary genotyping data. This showed one predominant MLVA type in aborted goats that was also found in diseased humans (Roest et al., 2011a, Klaassen et al., 2009). Additional analyses showed one predominant genotype in humans, which was the same as in goats (Tilburg et al., 2012).

As goats were the suspects of the human Q fever outbreaks, increasingly strong measures were imposed to prevent the spreading of C. burnetii in the lambing season. The first measures were implemented in 2008. These consisted of the notification of abortions in small ruminant holdings, hygiene measures, especially on manure handling, and a voluntary vaccination. In 2009, the measures were extended with tighter notification criteria, a transport and breeding ban and a mandatory vaccination. All of these measures, however, did not prevent the increase of human cases in 2009. Ultimately, to stop the increase of human cases the drastic decision was taken in 2010 to eliminate all potential high-risk animals. This resulted in the culling of all pregnant goats on Q fever positive farms. All of these measures finally resulted in a decline in human cases in 2010.

2.2. Probable causes of the outbreak

What exactly caused the Dutch Q fever outbreak? Epidemiological and genotyping investigations confirmed dairy goats and sheep as the cause of the human outbreak. But what caused the Q fever problems in goats? Q fever had been present in animal husbandry in the Netherlands for a long period of time and so it was not a new disease for the Netherlands. Several factors are hypothesised to have played a role. First, the strong increase in the number of dairy goat herds and goat numbers in recent years. In the 10 years prior to the outbreak, the number of dairy goats more than doubled and the herd size gradually increased to up to 900 animals on average. This increase could have influenced the in-herd dynamics of C. burnetii leading to problems. The partly closed status of some herds to prevent infectious diseases like paratuberculosis and caseous lymphadenitis could have made a herd more susceptible for C. burnetii or new strains of this bacterium. Second, the new introduction of a more virulent strain or a genetic shift to a more virulent strain could have caused the outbreak (Roest et al., 2011b).

3. Lessons learned

Q fever is a zoonosis that emerged from an endemic state in the Netherlands. Although several researchers had identified Q fever as a neglected disease in the Netherlands (Richardus, 1998) not much attention was paid to this by policymakers and funding bodies. Consequently, diagnostic tools and knowledge about the disease and its prevalence in humans and animals were not kept up to date. This hampered the early response to the outbreak and the confirmation of epidemiological links between humans and the source of the outbreak by genotyping. Genotyping systems had to be implemented and harmonised in human and veterinary laboratories so that results could be exchanged.

As this was the first large Dutch outbreak of a zoonosis, policymakers, disease control managers and researchers from the human and veterinary domain did not cooperate as a matter of course at the start of the outbreak. Furthermore, there were key differences in the response structure of the human and veterinary domains: in the human domain the response structure is strongly decentralised while in the veterinary domain it is centralised around the Ministry of Agriculture.

The most important lesson learned from the Dutch Q fever outbreak is that a close cooperation between the human and veterinary fields is essential for responding to outbreaks of zoonotic diseases. Specific disease knowledge and diagnostic tools from both fields are needed to manage outbreaks. Personal contact between policymakers, outbreak managers and researchers from both fields hugely facilitates the control of the outbreak. The Q fever outbreak evaluation committee (Evaluatiecommissie Q-koorts, 2010) reached these same conclusions. They also proposed a new early warning system to identify early signals of new emerging or re-emerging zoonosis. This signalling forum has been implemented and meets
monthly. It has already made a valuable contribution in the outbreak management of the Schmallenberg virus outbreak, for example.

4. Added value to the One Health approach

Experience from the Dutch Q fever outbreak clearly shows the inevitability of the human-veterinary cooperation in combating zoonotic diseases. During outbreak situations in particular, policymakers, outbreak managers and researchers from both sides need to trust each other and rely on each other’s research results. Personal contact shortens communication lines, which benefits the management of outbreaks. The management of the Q fever outbreak has demonstrated the benefits of the One Health approach. This approach is now implemented in the nationwide zoonosis structure.

5. Conclusion

In conclusion, Q fever in the Netherlands emerged from a dormant endemic state to outbreak proportions. Due to the dormant endemic state there was a lack of knowledge and diagnostic tools at the start of the outbreak. Genotyping of causative *C. burnetii* bacteria confirmed the epidemiological links between humans and dairy goats. The outbreak management needed an integrated human veterinary approach. This One Health approach is now leading in the signalling of emerging and re-emerging zoonosis in a national zoonosis structure.

References


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