





# From Q fever control to Psittacosis prevention

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#### Introduction

The Q fever epidemic in the Netherlands, from 2006 to 2010, is the largest Q-fever outbreak ever reported with 4,250 notified human cases and an estimated number of more than 50,000 infected persons. Dairy goats and dairy sheep were the source of the outbreak and this resulted in culling of 58,150 pregnant goats and 848,906 vaccinated dairy goats and dairy sheep (Figure 1).

Key in the control of the outbreak identification of the source by molecular confirmation of the epidemiological links between human cases and goat farms. Furthermore dataexchange between the human and animal health chain was vital for a timely response.

These lessons are now applied in an ongoing study on the zoonotic disease Psittacosis. Psittacosis is caused by the bacterium *Chlamydia psittaci* and can lead to a severe pneumonia in humans similar to Q fever. The disease is notifiable, but underreported, in humans and pet birds. The bacterium can be further subdivided genotypes based on its outer membrane protein A gene (ompA). The genotypes are associated with different bird hosts, which aids source finding.

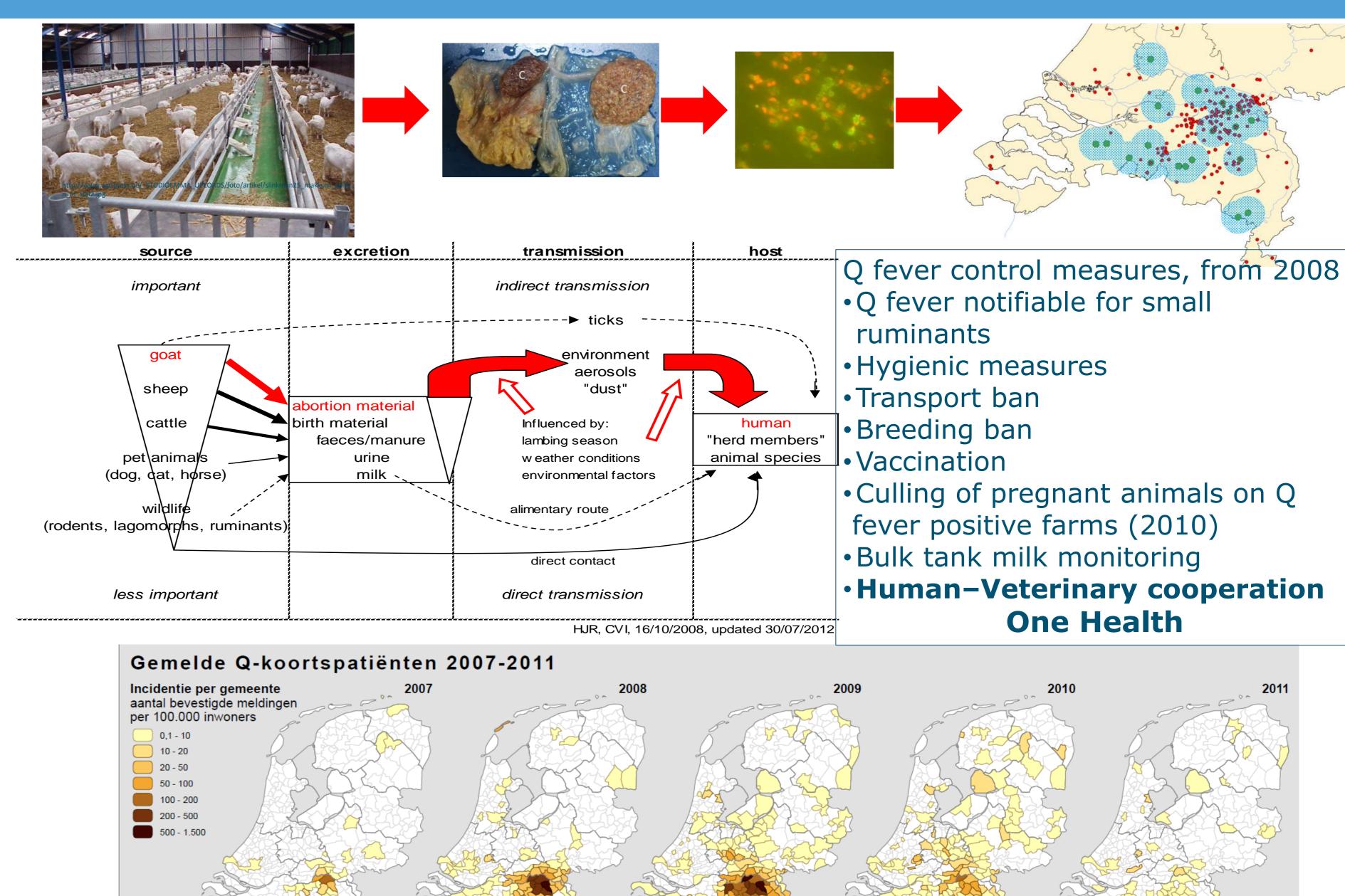


Figure 1. Summary of the Dutch Q fever outbreak.

**Objective** Establishing a 'One Health' data exchange platform that connects human cases to animal sources via clinical, epidemiological and genotyping data for the underreported zoonotic disease psittacosis.

### Methods

• identifying existing data and data sources of psittacosis • designing a web-based platform to incorporate all available data (Figure 2) • Designing an OmpA typing tool to facilitate genotype comparison of human- and animal C. psittaci isolates (Figure 2) • Overcome legal barriers on database use in relation to privacy legislation • Additional research was initiated to increase knowledge on the prevalence of *C. psittaci* in human and animals in the Netherlands.

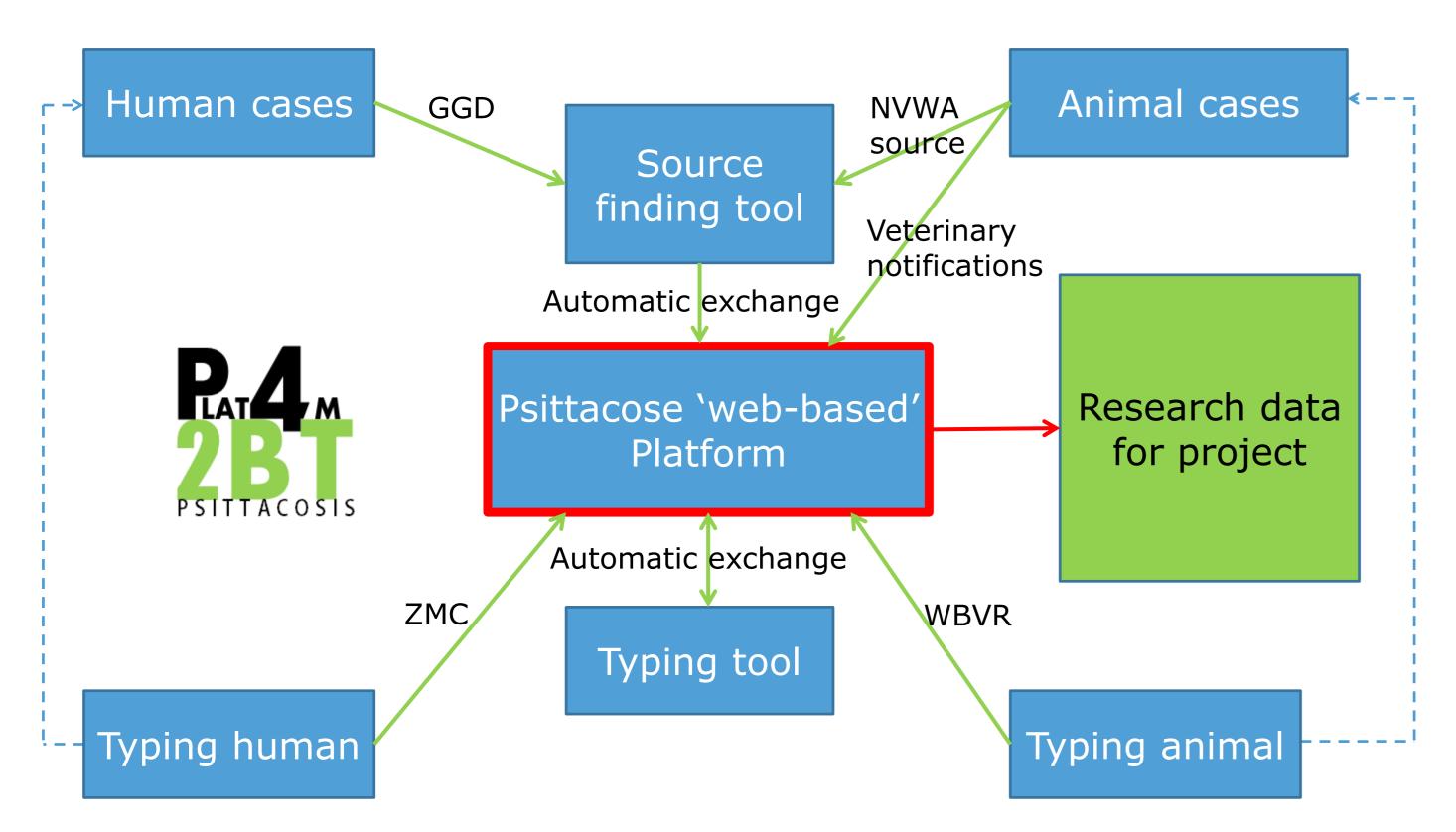


Figure 2. Overview of the integration of human and animal data in the web based platform to facilitate source identification of human psittacosis cases. GGD: municipal public health service; NVWA: Food Safety Authority; ZMC: Zuyderland Medical Centre; WBVR: Wageningen Bioveterinary Research.

### **Results & Conclusions**

- A prototype web-based platform and typing tool was established including automatic exchange with existing databases.
- Legal issues on database use to meet privacy regulations were complex and demanding. This hampered the progress of platform use and the project. Special attention should be given to database legal issues.
- A first assessment of psittacosis in Dutch layer farms indicate that C. psittaci is not present on these farms.
- Exploratory spatial analysis of human psittacosis notifications in the Netherlands showed a large cluster that covered a highly poultry-dense area but also the presence of additional clusters in areas that had a low poultry density.

## **References & Acknowledgements**

**Heijne M**, et al. A cross sectional study on Dutch layer farms to investigate the prevalence and potential risk factors for different Chlamydia species. PLoS One. 2018;13(1):e0190774. Hogerwerf L, et al. Temporal and spatial analysis of psittacosis in association with poultry farming in the Netherlands, 2000-2015. BMC infectious diseases. 2017;17(1):519.

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