A timely and coordinated response to zoonoses requires a systematic exchange of data between public and veterinary health. Source finding and assessment of the human transmission risk both require a matching of aetiological zoonotic pathogens of humans to their potential animal sources.

Although many lessons have been learned from two zoonotic outbreaks in the Netherlands (Avian Influenza and Q fever), a platform to exchange data and laboratory results between the public and veterinary health domains is still lacking. In this project, a ‘one health’ web-based framework that facilitates the exchange of epidemiological, clinical and molecular data from both human and animal cases of psittacosis will be constructed, evaluated and implemented to improve source finding by infectious disease control professionals.

Psittacosis, a notifiable disease in humans as well as animals, is underreported in humans and the relative risk of different bird species to human disease is unknown. This is particularly important for Dutch poultry, as this sector represents about 100 million birds and high prevalences of C. psittaci are reported in the literature. The overall aim of the project is to reduce the disease burden of psittacosis. In this multidisciplinary project, local infectious disease experts, microbiologists and researchers from both public and veterinary health will work together.

Firstly, we will develop an integrated human-veterinary data exchange platform that includes a ‘one health’ typing tool for Chlamydia psittaci to be used in the human and veterinary domains. Secondly, we will implement a ‘one health’ typing method for C. psittaci based on the current ompA sequence typing method that will be harmonised for use in both human and veterinary laboratories. A quality assurance system will be implemented using reference strains and sequence data added to the database will be checked by a curator to ensure the necessary quality is maintained. Thirdly, we will determine the presence and prevalence of C. psittaci in animal populations, including the poultry sector, pet birds and free-living birds. Fourthly, we will reduce the diagnostic deficit of psittacosis in humans by implementing a harmonised respiratory diagnostic PCR method in medical
microbiological laboratories (MMLs). Fifthly, we will determine the disease burden in humans, map psittacosis incidence and genotypes in animals and humans, and identify the main animal reservoirs for zoonotic transmission. And sixthly, we will evaluate the utility of the web-based platform using reported human and animal cases and implement the platform for source finding by public and veterinary health professionals.

These objectives will be organised in seven work packages of which six are research based. Interdisciplinary cooperation between local and national infectious disease experts will be realised through molecular biologists, diagnosticians and infectious disease control professionals from the domains of public and veterinary health working together in this project.

Careful coordination of all parties involved and the sharing and evaluation of actions during the project are vital to the project’s success. Specific attention has therefore been paid to the management of the project and the dissemination of the results obtained. This will be realised in a seventh work package coordinated by two project leaders from the public and veterinary health domains who will work closely together. The exchange of experiences and new results obtained in this project will lead to improved knowledge about psittacosis among infectious disease professionals. Diagnosis and source finding of psittacosis will be improved, which will eventually lead to a reduced disease burden of human psittacosis. Successful implementation of the platform to beat psittacosis in this project will provide a proof of principle to control other notifiable and emerging zoonoses in the future using a similar approach.