



## Hot topic

## New evidence for domesticated animals as reservoirs of *Chlamydia*-associated community-acquired pneumonia

Recent reports of cases of community-acquired pneumonia (CAP) from around the world have brought increasing recognition to the zoonotic potential of an expanded range of obligate intracellular bacteria in the genus *Chlamydia* that are typically only associated with infections in animals.

The most surprising of these cases was documented recently in The Netherlands [1]. In this report, three unrelated cases of human infection by *Chlamydia caviae* were reported in individuals experiencing severe atypical pneumonia following exposure to ill guinea pigs. The natural host of *C. caviae* is thought to be guinea pigs, although molecular studies have also detected it in other domesticated animals, including cats and rabbits [2]. Two of the three patients required admission to an intensive care unit. Molecular typing confirmed the presence of the same strain in both bronchoalveolar lavage fluid from one patient and her guinea pig. A separate Dutch case of *C. caviae*-associated CAP was also recently described [3]; however, no direct animal exposure was detected in this case.

New reports of unusual presentations of chlamydiosis are not limited to humans. A recent study found that >20% of pregnancy losses and early foal deaths in horses were positive for *Chlamydia psittaci* [4]. *C. psittaci* is an avian pathogen that can also cause serious atypical pneumonia in humans, known as psittacosis. Zoonotic transmission is thought to be mediated by direct and indirect contact with birds; however, in 2014, a cluster of human cases of psittacosis was documented involving contact with the *C. psittaci*-infected placental material from a mare [5]. This case represented the first confirmed example of mammal-to-mammal transmission of *C. psittaci* and, in the context of this most recent equine investigation, would suggest that the risk of human exposure from veterinary chlamydiae causing CAP is more substantial than previously estimated.

These reports point to the potential for an underestimation of CAP because of chlamydiae, particularly those resulting from exposure to veterinary chlamydial pathogens from unexpected sources. Indeed, a Dutch study estimated that ~1% of the total number of hospitalized cases of CAP were caused by *C. psittaci*, resulting in 503 cases, rather than the 93 actual notifications reported in the period 2008–2011 [6]. The likely explanation for this discrepancy is that most cases of CAP are treated without diagnostic testing in general and/or that tests with specificity for veterinary chlamydiae were not applied. Improving the detection of chlamydia-associated CAP, as such, requires careful consideration of the practice and

policies to support primary-care physicians, infectious disease specialists, and public health authorities to work in partnership with veterinarians.

An example of such an overarching 'One Health' partnership for chlamydia-associated CAP surveillance has been developed in The Netherlands in the aftermath of the largest outbreak of Q fever between 2007 and 2010 [7]. Lessons from this outbreak informed the creation of a One Health platform for psittacosis, designated Plat4m-2Bt-psittacosis [8] (<https://www.wur.nl/en/Research-Results/Research-Institutes/BioVeterinary-Research/Projects/Show/Plat4m-2Bt-psittacose-1.htm>). One of the key components of this platform has been the harmonization of both molecular detection and typing methods to enable an easy exchange of human and animal chlamydial sequence data between laboratories to support source tracking between animal and human public health authorities. For *Chlamydia* detection in diagnostic specimens (e.g. sputum, nasopharyngeal swab) from patients with suspected CAP, we recommend either (1) a sensitive quantitative PCR assay that targets several of the veterinary chlamydiae now described in association with community acquired CAP [9]; and/or (2) a PCR assay with a broader host range to detect existing but potentially undescribed *Chlamydia*-related bacteria [10–13]. Subsequent positive results can then undergo urgent molecular typing using established schemes [1,4,14] to not only confirm the suspected chlamydial species but also to direct further efforts to identify the potential animal infection reservoirs. In doing so, this two-step approach is anticipated to improve the overall surveillance of chlamydia-associated CAP while continuing to reveal new and fascinating examples of chlamydial zoonoses that are of concern to human and veterinary clinicians alike.

### Transparency declaration

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