

New and emerging chlamydial infections of creatures great and small

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Abstract

Until recently, our knowledge of the host range and diversity of members of the *Chlamydiaceae*, obligate intracellular bacterial pathogens of humans and animals, was thought to be nearly complete. Aided by advances in molecular diagnostics, a new picture is emerging, however, that the host barriers may be looser than previously thought for many chlamydial species. While cross-host transmission of chlamydial species is a concern for animal health, new reports highlight an emerging zoonotic risk for several species associated with intensification of farming and the widespread popularity of companion animals. The description of an expanded cohort of new species within this family from avian and reptilian hosts has also highlighted how much we still have to learn about the biology and pathogenicity of the *Chlamydiaceae* as a whole. Reports emerging about these relatives of the traditional chlamydial pathogens are matched by the continued identification of novel *Chlamydia*-related bacteria in the phylum *Chlamydiae*, providing evidence that many may be pathogenic to humans or animals and pose a zoonotic or vector-borne risk. The review examines the new hosts described for well-characterized chlamydial veterinary pathogens, emerging novel chlamydial species and the potential for these to cause disease in their respective hosts.

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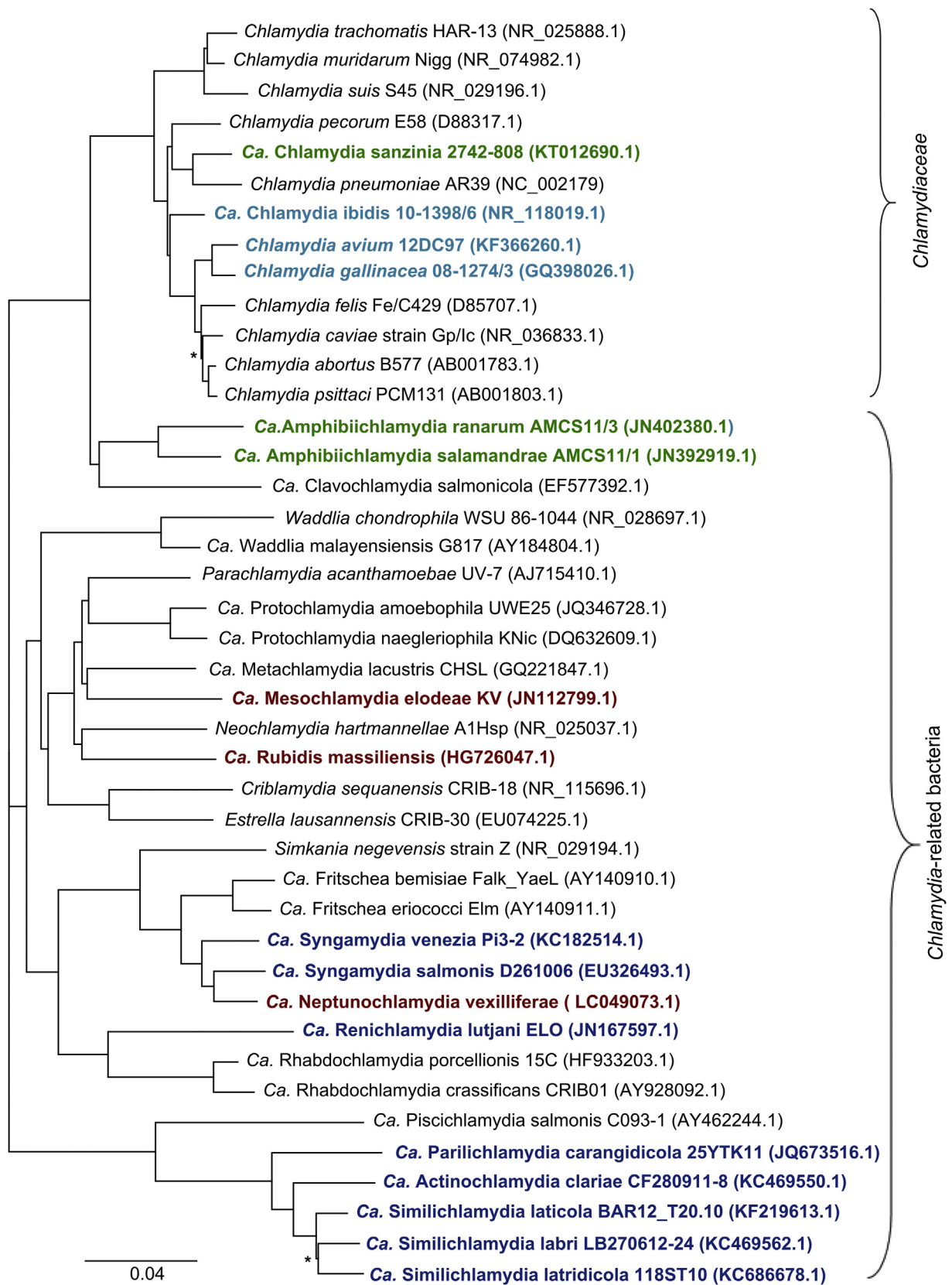
Introduction

Bacteria in the family *Chlamydiaceae* are globally significant human and animal pathogens. Until recently, the *Chlamydiaceae*, the best-characterized family in the phylum *Chlamydiae*, comprised nine taxonomically recognized, well-defined species belonging to the genus *Chlamydia*: *C. trachomatis*, *C. muridarum*, *C. suis*, *C. psittaci*, *C. abortus*, *C. caviae*, *C. felis*, *C. pneumoniae* and *C. pecorum* [1]. This view has begun to rapidly change with the discovery and description of two novel chlamydial species and two *Candidatus* species in avian and reptile hosts: *C. avium*, *C. gallinacea* [2] and *Candidatus C. ibidis* [3] from domestic and wild birds and *Ca. C. sanzinia* from a captive snake [4]. Outside of

this well-described family, wider sampling and advances in molecular methods have revealed a breadth of novel families within the phylum [5], collectively referred to as *Chlamydia*-related bacteria (CRBs) because of their phenotypic and genetic similarities but phylogenetic separation from the *Chlamydiaceae*.

The detection of emerging infectious diseases has been steadily increasing over the last 70 years and predominantly comprises zoonoses from wildlife [6], with wildlife species richness being a predictor for the emergence of zoonotic diseases with a wildlife origin [6]. The intensification of farming and widespread popularity of companion animals also present ongoing opportunities for emerging zoonoses [7]. Whilst improvements in surveillance and diagnostics have contributed to a wider recognition of the emergence of these pathogens [7], anthropogenic factors such as antimicrobial use, agricultural practices and human population density are drivers of emerging infectious diseases in general [6].

This review examines the new animal hosts described for well-characterized chlamydial veterinary pathogens, emerging novel chlamydial species and their potential to cause disease in humans, animals or both. We have limited our review to the



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