Chlamydia in birds - occurrence, new species and zoonotic potential – a review

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Abstract

Chlamydiae, one of the oldest bacterial orders in evolutionary terms, are widespread among animals. Blinding trachoma, a disease caused by Chlamydia trachomatis, was already known in ancient times, whereas modern reports on psittacosis date from 1879. Though these pathogens have long been known and lead to serious health problems both in human and animals, data on Chlamydiales biology has been limited. It is due to their intracellular life style and complex developmental cycle. New molecular biological methods have been recently developed expanding the possibilities of chlamydial research and diagnosis. This paper reviews data concerning avian chlamydiosis, its aetiological agent C. psittaci, newly proposed species isolated from birds, namely C. ibidis sp. nov., C. avium sp. nov., and C. gallinacea sp. nov., and their zoonotic potential.

Keywords: avian chlamydiosis, zoonotic potential, C. psittaci, atypical strains.

Introduction

A wide variety of species within the vertebrates, arthropods, and even amoeba can be hosts for a diverse group of Chlamydiaceae (49). The disease caused by these bacteria was already known in ancient times, as the first historical description of trachoma (blinding disease) was found in the Ebers papyrus dated around 1550 BC (4). Nowadays, it has been proved that Chlamydia are the cause of numerous diseases in man and animals, i.e. human infectious blinding trachoma or sexually acquired infections (Chlamydia (C.) trachomatis), enzootic abortion in ewes (C. abortus), or ornithosis in birds (C. psittaci) (20, 49). The diseases are of enormous importance in view of both public health, including general health care programmes, and economic losses in livestock production. Some chlamydial agents of veterinary interest, like C. psittaci or C. abortus, have also displayed zoonotic potential (8, 28).

Chlamydiaceae are extremely interesting due to their specific biphasic life cycle developed in their distant evolutionary past. Most probably they were one of the first to divide from the bacteria trunk around 2000 million years ago (21). At that time, the present-day hosts were not yet available, so a single-celled eukaryote was most probably the first organism to be conquered. Some features typical for all Chlamydiaceae had to have evolved before the divergence of families (most probably about 1000-700 million years ago) and species as characteristics of the last common ancestor (4, 16). One of these would be the strictly intracellular, mainly parasitic existence and developmental cycle of division between infectious (elementary body – EB) and reproductive (reticulate body – RB) cell types. At the end of the cycle proliferation occurs within vacuoles forming chlamydia-packed inclusions. Typical for all Chlamydiaceae (with small exceptions) are also reduced genome size (around 1 Mbp), from 80% to 90% 16S r RNA sequence similarity, and negative Gram staining (20).

Up to 1999, Chlamydiaceae were a phylum with one family, Chlamydiaceae, and four species, namely C. trachomatis, C. psittaci, C. pneumoniae, and C. pecorum. Then, Everett et al. (10) suggested a major change within the order based on an analysis of 16S r RNA sequence similarity. Firstly, three additional families were added, and secondly, the genus Chlamydia was divided into two genera - Chlamydia and Chlamydophila, and five additional species in the Chlamydiaceae family were proposed. Currently, as more molecular data is gathered, the chlamydial taxonomy as
summarised by Horn (20) is widely applied. This matter was discussed earlier (49). The paper will focus on the Chlamydiaceae infectious to birds, which are C. psittaci and the newly proposed species, on the occurrence of mixed infections, and on the zoonotic potential of Chlamydia.

**Avian chlamydiosis.** C. psittaci was the next species of Chlamydiaceae family identified after C. trachomatis. The disease caused in humans by C. psittaci was firstly recorded by Jacob Ritter in 1879 (32) when he reported pneumonia acquired from parrots. In the next decades some cases of psittacosis were observed, the disease being most virulent in an outbreak in Europe and America at the end of the 1929 and the beginning of the 1930, with 766 cases and 112 fatalities. Until that outbreak no extensive research had been done on the subject (32). Description of the bacterium in 1930 by three researchers independently, who were Levinthal, Coles, and Lillie, enabled a further progress on the knowledge of biology of this pathogen (32).

C. psittaci is widespread among wild and domestic avian species. According to Kaleta et al. (22), 469 bird species from 30 orders were found positive for this pathogen by isolation of the agent, antigen detection, or serological examination. The disease caused by C. psittaci was known as psittacosis or parrot fever when concerning psittacine birds, or as ornithosis in other avian species. Both terms are now used interchangeably together with the appellation “avian chlamydiosis”. Variants vary greatly from asymptomatic to systemic infection with fatal outcome. Clinical symptoms can include loss of condition, anorexia, fever, diarrhoea, respiratory problems, nasal and ocular discharges, and lethargy. Conjunctivitis, pericarditis, sinusitis, airsacculitis, pneumonia, lateral nasal adenitis, peritonitis, hepatitis, and splenitis are also observed (1, 17, 28, 39). The severity of infection depends on the chlamydial strain as well as on the species, age, and general condition of the bird. Mortality can vary again depending on the same factors but can sometimes reach even 80%. Inhalation of aerosolised droppings, respiratory exudate, and dust are the main transmission routes (17). Chronic infection with no clinical signs is very often reported and clinical manifestations start usually as a result of stress i.e. transportation, overcrowding, and poor nutrition (43). Even though no signs of infection are observed, the animal can still be a heavy shedder of the agent contributing to the spread of the disease (17).

For a long time, C. psittaci was thought to be the only chlamydial infection agent in birds and at the same time one infecting predominantly avian species albeit that transmission to people was also known, which will be discussed later. However this point of view has changed in recent years when more data has been available. Other Chlamydiaceae species, like C. abortus, C. trachomatis, and C. pecorum, were detected in brown skua, parrots, parakeets, and pigeons (19, 30, 36). Infections of non-avian species with C. psittaci are also often reported. Lenzko et al. (27) showed the presence of C. psittaci in 25% of clinically healthy sheep flocks tested. Mixed infections with C. abortus or C. pecorum were interesting findings. Reports of C. psittaci occurrence in cattle are numerous around the world (3, 23). Sometimes this agent is the most prevalent species (24), Vanrompay et al. (45) summarised cases of its detection in different animal species, i.e. pigs, goats, horses, koalas, but also Nile crocodiles and African clawed frogs.

**Newly described species.** The development of very specific molecular biology methods enabled further progress in chlamydial diagnostics and research. DNA-based detection is rapid, specific, and reliable. The usual targets include an RNA operon or the outer membrane protein A (ompA) gene allowing genus and species differentiation. Chlamydiaceae-specific detection protocols for both conventional (9, 29, 34) and real-time PCR (5, 7, 11) were published and are widely used. Species-specific assays for chlamydia of veterinary interest, including C. psittaci, are also available (14, 30). New technologies like microarray platforms were also employed in Chlamydia sp. detection and the genotyping of C. psittaci (35, 37).

Thanks to the development of these techniques, atypical strains of Chlamydiaceae were detected in poultry, pigeons, and ibises. The occurrence of new chlamydial species was first described in Germany in 2008 (12) in connection with a psittacosis outbreak, and later on in France by Laroucau et al. (26) following cases of atypical pneumonia in slaughterhouse workers. These were followed by further reports from different countries around the world (2, 13, 33, 36, 41, 48, 50, 51).

As a result of extensive investigations, including agent isolation, multilocus sequence analysis (MLSA), whole genome sequencing, and phylogenetic analysis, new species in the Chlamydiaceae family were proposed. These comprise C. ibidis sp. nov., C. avium sp. nov., and C. gallinacea sp. nov., which were isolated from birds.

C. ibidis was described by Vorimore et al. (48) in 2013 in samples from the feral sacred ibis (Threskiornis aethiopicus) population living in southern and western France. Research was performed during a cull as ibises are considered an alien and invasive species in this area, with a possible impact on biodiversity and representing a probable pathogen reservoir. Strain isolation and characteristics as well as a detailed molecular analysis led to the description of a 1.15 Mbp chromosome of C. ibidis sp. nov. with 1057 predicted coding sequences. Intracellular growth characteristics were also confirmed, with two distinct developmental forms (EB and RB), which are in line with Chlamydia sp. description (20). The 16S rRNA sequence of 95% similarity or greater with all nine chlamydial species meets the specification for genus assignment. The highest score of 99.86% for C. psittaci 6 BC strain shows C. ibidis as the closest relative. A feature specific to this species is the lobar shape of the nucleoid observed in the EB form. Until now, C. ibidis has only been found in ibises but it is not excluded that it can infect other avian or mammalian species.
C. avium was isolated from pigeons and psittacine birds (38, 51) but it is probable that other species could also serve as its host. Most cases of infection are asymptomatic but pathogenicity cannot be ruled out. Sequencing revealed that its genome of 1.04 Mbp, with 949 annotated proteins, is one of the smallest in the family but comparable with that of C. trachomatis. C. avium shows typical morphology while propagated in cell culture with growth within inclusions surrounded by mitochondria and Golgi membranes. The life cycle of about 60-72 h with changes between EB and RB forms also closely resembles that of other Chlamydiales. Comparison of 16S rRNA showed the highest sequence homology with the newly proposed C. gallinacea and also high homology with C. psittaci (98.2% and 98.05% respectively) (38).

C. gallinacea was exclusively isolated from domestic poultry samples (i.e. chicken, turkey, and quail) (38). The genome size is 1.05 Mbp, in which 899 coding sequences were predicted. The highest 16S rRNA sequence homology was demonstrated with C. avium (98.7%) and C. psittaci (98.1%). The species description, as for C. avium, is in full agreement with Chlamydiaceae family phenotypic and genotypic characteristics. An MLSA assay performed on four loci showed that C. gallinacea is more heterogeneous, as three different sequence types (ST), in comparison with only two for C. avium, were identified. Different plasmid sequences were found in both type strains (38).

Zoonotic implication of C. psittaci and new species. Psittacosis can be transmitted to humans by direct contact with infected birds or their discharges (46). C. psittaci is considered to have the greatest zoonotic potential in the Chlamydiaceae family. The highest possibility of acquiring chlamydial infection adheres to occupational risk groups like pet owners, breeders, veterinarians, farm workers, or poultry meat processing plant employees exposed to repeated contact with birds. Psittacine birds, pigeons, and waterfowl, as well as chicken, turkeys, ducks, and other poultry constitute the main hazard (6, 18, 31, 42, 47). The length of the incubation period differs from 5 d to 14 d and sometimes longer (17). After this time, flu-like symptoms, including fever, chills, and headache, usually occur. Further progression to pneumonia is frequent. The course of chlamydiosis ranges from asymptomatic through mild symptoms to severe and systemic illness. Corollary complications such as endocarditis, myocarditis, hepatitis, arthritis, keratoconjunctivitis, encephalitis, renal disorders, and miscarriages in pregnant women are also reported (15, 25, 40, 45). Tetracyclines (doxycycline and tetracycline) are the drugs of choice in psittacosis treatment, with macrolides, mainly erythromycin, as the alternative in individuals where use of tetracyclines is not recommended (children and pregnant women) (28, 40). Antibiotic therapy is recommended for at least 10-14 d, as otherwise relapses are common. The mortality rate is low with proper treatment, but due to unspecific clinical signs diagnosis is difficult. It is supposed that the actual prevalence of psittacosis in humans is underestimated, because of both misdiagnosis and the quite often unapparent nature of infections (18, 44, 46).

Available data shows that some of the new species, especially C. avium and C. gallinacea, may be widely disseminated. Though both of them were detected mainly in asymptomatic birds, a pathogenic role and zoonotic potential were suggested (26, 38) and further investigation is needed.

References


