CHLAMYDIALES – TAXONOMY, PATHOGENICITY, AND ZOONOTIC POTENTIAL

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Abstract

Changes in the taxonomy of the order *Chlamydiales*, after its separation from the order *Rickettsiales*, were presented. These changes resulted in the recognition of the following families: *Chlamydiaceae*, *Chlavichlamydiaceae*, *Criblamydiaceae*, *Parachlamydiaceae*, *Piscichlamydiaceae*, *Rhabdochlamydiaceae*, *Simkaniaceae*, and *Waddliaceae*. Other described changes concerned particularly the family *Chlamydiaceae*. Its genus *Chlamydia* was divided into *Chlamydia* and *Chlamydophila*. However, in the following years, a revision to the single original genus was made, based upon phylogenetic analysis of 16S and 23S rRNA genes of the strains belonging to these two taxonomic units. The review also discusses other families outside the family *Chlamydiaceae*, which contain so-called *Chlamydia*-related or *Chlamydia*-like organisms. Members of each family share a 16S rDNA gene sequence similarity >90%. Furthermore, characterisation of the pathogenicity is presented, focusing especially on the representatives of the family *Chlamydiaceae*, which cause animal infections, and describing their zoonotic potential. Available data on this topic, connected with the representatives of other families, were mentioned.

Key words: *Chlamydiales*, taxonomy, pathogenicity, zoonotic potential.

Data available in the Polish literature on creating the order *Chlamydiales*, can be found in the publications by Pawlikowska and Deptula (27) and Truszczyński (40). At the beginning, type *i.e.* phylum *Chlamydiae* consisted of one family *Chlamydiaceae* separated from the order *Rickettsiales* into the created order *Chlamydiales*, according to Bergey (6). Based on the study of Wheelhouse and Longbottom (43), that resulted in re-classification of the *Chlamydia* in 1999, Everett *et al.* (13) displayed the data on creating four separate families within the order *Chlamydiales*, namely: *Chlamydiaceae*, *Parachlamydiaceae*, *Simkaniaceae*, and *Waddliaceae*. The authors introduced division of *Chlamydia* into two genera: *Chlamydia* and *Chlamydophila*, which was commonly accepted until recent years. Moreover, apart from four existing species: *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Chlamydophila psittaci*, and *Chlamydophila pecorum*, they presented conclusions on creating five additional species: *Chlamydia suis*, *Chlamydia muridarum*, *Chlamydophila abortus*, *Chlamydophila felis*, and *Chlamydophila caviae*, within the concept. The division was based on phylogenetic analysis of the genes 16S and 23S rRNA (43). It was additionally supported by phenotypic, morphological, and genetic properties of the microorganisms (43).

The above mentioned data were accepted by bacteriologists worldwide. In 2009, however, Stephens *et al.* (36) contested grounds for retaining the gender *Chlamydophila*. As a reason for re-connecting the two taxonomic units in one genus, the cited authors

presented results of the comparative analysis of the genome of *Chlamydia* and *Chlamydophila* strains isolated from different hosts. The analysis revealed significant similarities among the studied strains, apart from several exceptions (Fig. 1). In 2011, these results were confirmed by Horn (20). Wheelhouse and Longbottom (43) presented the reversion to initially one genus *Chlamydia*, including nine currently known genera of the family *Chlamydiaceae*: *Chlamydia* (*C.*) *trachomatis*, *C. muridarum*, *C. suis*, *C. pneumoniae*, *C. psittaci*, *C. abortus*, *C. caviae*, *C. felis*, and *C. pecorum* (20).

Fig. 1. *Chlamydia* species names showing percentage of 16S rRNA gene similarity between species (36).

Apart from the typical *Chlamydia* belonging to the family *Chlamydiaceae*, seven families including *Chlamydia*-related or *Chlamydia*-like organisms were created (43). Representatives of the families were characterised by the 80%-90% similarity of the 16S rDNA, sequence with *Chlamydiaceae*. Affinity to the family was based on the similarity higher than 90% of the gene sequence 16S rDNA of the particular strains. The names of the families and corresponding genera and species as well as typical hosts (43) appear as follows: *Candidatus Clavichlamydiaceae* with the genus *Candidatus Clavichlamydia* and the species *Candidatus Clavichlamydia Salmonicola* - the main host salmonids; *Criblamydiaceae* with the genus *Criblamydia* and the species *Criblamydia sequanensis* and *Estrella lausannensis* occurring in the fluvial water; *Parachlamydiaceae* with the genus *Parachlamydia* and the species *P. acanthamoebae* - the main host *Acanthamoeba*. *Neochlamydia* with the species *N. hartmannella* - the main host *Hartmannella vermiformis*, belongs to the family as well. The third genus of the family is *Protochlamydia* with the species *Candidatus P. ameobophila* - the host *Acanthamoeba*. *Candidatus P. naegleriophila* - the host *Naegleria amoeba* also belongs to the genus. The following family is *Candidatus Piscichlamydiaceae* with the genus *Piscichlamydia* and the species *Candidatus Piscichlamydia salmonis*, which occurs in salmon farms in the Atlantic Ocean. Next family is *Rhabdochlamydiaceae* with the genus *Rhabdochlamydia* and two species: *Candidatus R. crassificans* - the host arthropods (cockroaches), and *Candidatus R. porcellionis* - the host wood louse. The following family is *Simkaniaceae* with the genus *Simkania* and species *S. negevensis*. The next genus of the family is *Candidatus Fritschea* with two genera: *Candidatus F. ericococci* and *Candidatus F. bernisiae* - the host insects. The eighth family including *Chlamydiaceae*, is the family *Waddliaceae*, with the genus *Waddlia* and the species *W. chondrophila* - host cattle, as well as the genus *W. malaysiensis* - host fruit bat.

The species from the family *Chlamydiaceae* can be characterised according to the degree of pathogenicity and zoonotic potential of *Chlamydiales*, which will be discussed in the next sections.

Among the species of the mentioned family, *Chlamydia psittaci* has the highest zoonotic potential. In birds it causes avian chlamydiosis. It occurs in true parrots (*Psittacoidea*), farm poultry, and wildfowl. Depending on the virulence of the infecting strains, the disease has acute or mild course in farm poultry. The infection can be asymptomatic as well, more frequently in older, rather than in younger birds (19). In *Psittacoidea*, increased internal body temperature, loss of appetite, diarrhoea, respiratory disorders, and conjunctivitis are frequently observed (30). In turkeys, serovar D of *C. psittaci* brings about exceptionally often the disease symptoms such as conjunctivitis, rhinitis, sinusitis, tracheitis, sacculitis, pericarditis, pneumonia, and enteritis. Persons having contact with poultry and ornamental birds are most exposed to the infection and disease. It concerns also personnel taking part in

slaughter of turkeys (and other birds), and processing their products (41). Despite the facts that chlamydiosis in ducks is mostly asymptomatic, ducks can also constitute a source of the disease for humans (25). In humans, period of incubation lasts 1-2 weeks, sometimes it can be longer. The symptoms of the disease are atypical, and they are manifested by mild flu-like illness with an increased body temperature, headache, catarrh of the mucous membranes of the nose and throat, myalgia, and diarrhoea. Intermittently, endocarditis, encephalitis, and pneumonia can occur, which sometimes leads to death (28). In pregnant women, the infections from birds can bring about miscarriages (21).

Chlamydia abortus is an aetiological factor of enzootic abortion of ewes as it is a microorganism causing the most frequently occurring abortions in small ruminants. The losses caused by the disease are significant (31). *C. abortus* brings about infections in cattle, swine, roe-deer, and horses. Additionally, it constitutes a determined zoonotic risk causing intermittently, mild flu-like illness or, rarely, pneumonia in humans. In pregnant women, it can cause miscarriages (22, 35).

Chlamydia felis causes conjunctivitis in cats and humans, what indicates its zoonotic properties (39). The species is also considered as a rare cause of pneumonia in human (8).

Chlamydia pneumoniae is mainly a human pathogen, infecting mostly the lungs. It can be a factor, *inter alia*, complicating Alzheimer's disease (1), coronary disease (5), and arthritis (18). *C. pneumoniae* can be isolated from animals including amphibians, reptiles, and mammals (37). Genome analysis showed that the strains of *C. pneumoniae* occurring in people had primarily the animal origin; however, currently they remain and spread in humans without animal reservoir's participation (26).

The natural host of *Chlamydia suis* is swine (14) in which the species provokes or co-provokes conjunctivitis, sinusitis, pneumonia, enteritis, and reproduction disorders expressed by increased mortality of embryos or foetuses, as well as repeating heats. *C. suis* has a negative impact on sperm quality by decreasing motility of spermatozoa or causing their dying. Pigs, however, are first of all asymptomatic carriers of *C. suis*. Within the species, a considerable diversity of genome and genotype properties of the particular strains, including capacity to co-creating different syndromes in swine, was demonstrated (34).

Chlamydia pecorum is defined as a microorganism, which can induce or co-induce pneumonia, conjunctivitis, arthritis, enteritis, mastitis, metritis, encephalitis, and myelitis in swine, cattle, and koala (38).

Zoonotic potential of *C. suis* and *C. pecorum* has not been sufficiently determined so far (43).

In the following section, the pathogenicity for animals and zoonotic potential of *Chlamydia*-related microorganisms, also belonging to the order *Chlamydiales*, will be characterised.

Waddliaceae. According to the data presented by Wheelhouse and Longbottom (43), twenty years have elapsed since the first isolation of *Chlamydia*-related microorganism from a case of bovine abortion in the USA (11). It was noted that the isolated organism had the life cycle similar to the representatives of *Chlamydiaceae* (23). Additionally, it caused bovine foetopathy. In calves not receiving colostrum, and in one-year-old goats, the infection caused temporary health disorders such as increased internal body temperature, leukopenia, and slowly developing but longer retaining anaemia (9). The classification using 16S rRNA gene analysis, determined the belonging of the germ to the order *Chlamydiales* with the name *Waddlia chondrophila* (33). Despite positive results in serological tests using the antigen *W. chondrophila* during the following years, participation of the organism in the abortions in cattle and calves was not confirmed (12). In 2011, three cases of abortions in cattle were noted in Switzerland, where *W. chondrophila* was identified with the use of RT-PCR and two of them were confirmed by immunohistochemical tests (3). Although this type of infections connected with abortions is sporadic, according to Wheelhouse and Longbottom (43), they occur more frequently than it is indicated in the documented and published data. Identification of the infectious causes of abortions in cows is not complete, when the identification of the germ is lower than 35% of cases, even when foetus and placenta are tested (7). *W. chondrophila* is presumably also a potential human pathogen. It multiplies in numerous kinds of human cells including macrophages as well as endometrium cells. It is assumed to participate in reproduction disorders in women (2). Moreover, it can take part in pneumonia in human (17) and inflammation of the upper respiratory tract in children (15).

Parachlamydiaceae. Recently conducted research with the use of molecular and immunohistochemical tests showed, according to Wheelhouse and Longbottom (43), the presence of the microorganisms of the genus *Parachlamydia* (4) in the cells of aborted bovine foetuses. The data were confirmed in Great Britain as well (10). However, to determine more precisely the role of the germs from the genus *Parachlamydia* in abortions in cattle, it is necessary to conduct research taking into account exclusively the microorganism and infections in pregnant cows. Only one publication indicates connection between *Parachlamydia* and abortions in small ruminants (32). The conducted tests identified the microorganisms only in 0.9% of examined goat samples. Swabs from eyes of sheep with conjunctivitis contained DNA of *Parachlamydia*, found also in swabs from eyes of healthy sheep (29). The strains *Parachlamydia* were detected in fluids from eyes of guinea pigs and cats (43).

More broad and precise studies were conducted on pathogenicity of *Parachlamydiaceae* in humans. At present, *Parachlamydia acanthamoebae* is considered as one of the pneumonia causes (16). DNA of *Parachlamydia* was identified in a number of cases of pulmonary diseases in newborns or complications related to the lungs in adults (24).

Rhabdochlamydiaceae. The family is represented by two species, which primarily were found in arthropods - *Rhabdochlamydia porcellionis* in woodlouse and *R. crassificans* in cockroaches. Recently, the microorganisms from the family *Rhabdochlamydiaceae* were isolated in 6% of samples from the cases of abortions in cattle (42). They are suspected to be responsible for pneumonia in humans and particularly in newborns (24).

In summary, this review presents the latest results of studies, conducted by a number of research groups, on the pathogenicity for animals and zoonotic properties of the representatives of the order *Chlamydiales* including mainly species of the family *Chlamydiaceae* and, to a lesser degree, *Chlamydia*-related families. The data obtained so far clearly indicate that the knowledge in this field is incomplete and requires further investigations. It is possible that the broadly understood environment, including water reservoirs with inhabiting animals, constitute reservoirs of the microorganisms from the characterised group, which can pass to domestic animals in a way that is still undetermined, and cause or co-cause diseases, which have not been assigned to these pathogens so far. Moreover, their zoonotic potential also has not been fully elucidated. Therefore, it is clear that further research on pathogenicity and zoonotic properties of *Chlamydiales*, as well as the studies aiming at improvement of their taxonomy are continuously necessary.

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