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RESEARCH ARTICLE
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Serological and molecular prevalences and phylogenetic analysis of *Coxiella burnetii* in dogs in Al-Qadisiyah and Baghdad Provinces, Iraq

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Abstract

Background and Aim: *Coxiella burnetii* is a highly contagious zoonotic bacterial micro-organism. This study aimed to estimate the prevalence of *C. burnetii* in dogs using serological and molecular methods. Furthermore, a sequencing analysis of *C. burnetii* dog isolates was conducted.

Materials and Methods: A total of 172 dogs, including 93 pet dogs, 21 police dogs, 38 guardian dogs, and 20 stray dogs, were selected. Venous blood was drained from the dogs and examined serologically by indirect enzyme-linked immunosorbent assay (ELISA) and molecularly by polymerase chain reaction (PCR) for *C. burnetii.* A sequencing analysis of *C. burnetii* dog isolates was conducted.

Results: The overall prevalence of *C. burnetii* was 16.86%, accounting for 55% in stray dogs, 9.68% in pet dogs, 19.05% in police dogs, and 13.16% in guardian dogs. Strong positive sera were observed in stray dogs (4.84 ± 0.29), whereas weak sera were observed in pet dogs (3.22 ± 0.18). PCR analysis revealed 6.4% positive dogs, accounting for 1.08%, 4.76%, 2.63%, and 40% in pet, police, guardian, and stray dogs, respectively. Phylogenetic tree analysis of local *C. burnetii* isolates revealed a total rate of similarity and mutations/changes between 95.47% and 100% and 0.059%, respectively. Subsequently, the local isolates were significantly similar to Chinese hedgehog, Iraqi camel, and Colombian human *C. burnetii* National Center for Biotechnology Information-GenBank isolates.

Conclusion: This is the first study on prevalence of *C. burnetii* in dogs in Iraq. To prevent transmission of *C. burnetii* to humans, the role of dogs or other domestic and wild animals as sources of infection must be investigated extensively. In addition, the prevalence of *C. burnetii* in other Iraqi regions should be surveyed using the most sensitive and specific diagnostic assays, such as ELISA and PCR.

Keywords: canine zoonotic diseases, *Coxiellosis*, polymerase chain reaction, Q-fever, sequencing analysis.

Introduction

Coxiella burnetii is an obligate intracellular, pleomorphic, Gram-negative, spore-forming, coccobacillary bacterium that belongs to the *Coxiellaceae* family, the *Legionella* order, and the *Gammaproteobacteria* phylum [1, 2]. This bacterium was first observed and isolated in Australia and the USA from 1920 to 1935. Although the morphological characteristics of *C. burnetii* are similar to those of *Rickettsia*, it exhibits some physiological and genetic variations [3–6]. This bacterium can also affect domestic and wild animals and humans, causing a disease known as Q fever or coxiellosis, which is endemic to several countries worldwide [7]. After infection, a large amount of *Coxiella* is excreted *via* milk, urine, feces, placenta, aborted fetuses, or reproductive tissues and then transmitted directly or indirectly to other animals or humans [8]. The inhalation of airborne materials, especially after animal birth, is a common cause of human infection [9]. In addition to mice and birds, more than 40 species of ticks have been found to play a role in the transmission of infection from animal to animal and from animal to human [7, 10]. Like intracellular micro-organisms, the acute phase produces antibodies that are provided by cellular response; in the chronic phase, high antibodies lead to the formation of immune complexes [6, 11, 12].

In dogs, *C. burnetii* infection is primarily characterized by the lack of symptoms or the presence of non-specific clinical symptoms, including depression, lethargy, seizures, and fever until the disease has progressed, thereby causing reproductive problems, such as stillbirth and deformities [13, 14]. Despite the development of a simple and reliable medium for screening *C. burnetii*, this bacterium remains an infectious organism [11, 15, 16]. Thus, enzyme-linked immunosorbent assay (ELISA), a sensitive, specific, ready-to-use, and commercially available diagnostic method, can be used to identify specific antibodies [17]. However, the correlation between