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**Study of circulating Leptospira strains in humans and dogs in mainland France, between 2019-2021: an unsuspected diversity.**

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Introduction
Leptospirosis is a widespread zoonotic disease caused by pathogenic bacteria of the genus *Leptospira*. The incidence of the disease continues to increase in mainland France and has exceeded 600 cases per year[1]. The key potential maintenance hosts are rodents, mainly rats[2], which excrete the bacteria in their urine and contaminate the environment. Humans and animals acquire the disease through direct contact with the urine of infected animals or indirect contact with contaminated environments. Both humans and dogs are susceptible hosts with comparable clinical manifestations ranging from febrile phase to multiple organ dysfunction[3]. Nevertheless, cases of leptospirosis in humans and dogs are most likely underestimated due to the lack of disease surveillance and limited epidemiological studies. Furthermore, the difficulty of obtaining isolated cultures limits our knowledge of the circulating strains. This study aimed to identify and describe the distribution of circulating pathogenic *Leptospira* ssp. in humans and dogs in mainland France, between 2019 and 2021, through the sequence polymorphism of the PCR products of the *lfb1* gene[4,5].

Methods
PCR assays for the detection of pathogenic *Leptospira* spp. were performed on samples from humans and dogs for which clinical manifestations of leptospirosis were reported between 2019 and 2021. Human samples were analyzed by the National Reference Center for Leptospirosis, and dog samples by the Veterinary Analysis Laboratory of VetAgro Sup. Only samples with a positive diagnosis were included in this study to identify the pathogenic *Leptospira* strain responsible for the acute infection. Sequencing of the *lfb1* gene amplification product was performed on 170 samples, including 110 human samples and 60 canine samples. Epidemiology data in particular vaccination status were collected.

Results
The phylogenetic analysis based on the *lfb1* sequence revealed a high genetic diversity within three *Leptospira* species: *L. interrogans* with seven *lfb1* species-groups (including 4 new *lfb1* species-groups), *L. kirschneri* with two *lfb1* species-groups (with 1 new *lfb1* species-groups) in humans and dogs; and *L. borgpetersenii* represented by one *lfb1* species-group in humans only. The *lfb1* species-group *L. interrogans* 1, corresponds to serovar Icterohaemorrhagiae or Copenhageni, was frequently retrieved (n=98/170; 57.6%) among human and dog cases. Furthermore, almost 50% (n=29/60) of the infected dogs included in the study had a complete vaccination profile against *Leptospira*, mainly with L4 vaccines (serovars Icterohaemorrhagiae, Canicola, Grippotyphosa, and Pomona) or L3 vaccines (serovars Icterohaemorrhagiae, Canicola and Grippotyphosa).

Conclusions
Our study presents, for the first time, a global picture of the *Leptospira* strains responsible for acute infections in humans and dogs in mainland France. It also shows the identification of five previously undescribed *lfb1* species-groups worldwide. We highly detected one *lfb1* species-group, *L. interrogans* 1, in both human and dog samples, suggesting that rats may be a common source of infection. It is worth noting from this study that the canine vaccinations currently available in France are only partially effective in preventing the clinical form of the illness.