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Diagnosis of acute leptospirosis in a dog by serological and molecular approaches - case report.

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Introduction: Leptospirosis, an important worldwide zoonotic disease, is recognized as a common cause of acute kidney disease in dogs (1). A significant hurdle to achieving a diagnosis is often the nonspecific clinical signs associated with leptospirosis, ranging in severity from no clinical signs to life limiting illness (2). The diagnosis of leptospirosis in dogs is commonly done through PCR on urine or blood, culture of urine or blood, or documenting a 4-fold rise in serum antibody titers over a 10-14 day period (3). While culture provides a definitive diagnosis, it can have low sensitivity due to the fastidious nature of Leptospira; and, because of the time required to obtain isolates, culture is seldom requested. Serologic studies in the U.S. showed that dogs were most often exposed to serogroups Autumnalis, Canicola, Icterohaemorrhagiae, Australis, Pomona and Grippotyphosa (4). Most acute cases of leptospirosis in dogs are attributed to Icterohaemorrhagiae (1). In this study, we report an acute clinical case of leptospirosis in a dog exposed to serogroup Pomona in the U.S.

exposed to serogroups Autumnalis, Canicola, Icterohaemorrhagiae, Australis, Pomona and Grippotyphosa (4). Most acute cases of leptospirosis in dogs are attributed to Icterohaemorrhagiae (1). In this study, we report an acute clinical case of leptospirosis in a dog exposed to serogroup Pomona in the U.S. Methods: A six-year-old female mixed-breed dog presented with vomiting, diarrhea, and lethargy. Her condition was monitored over 7 days. Blood urea nitrogen (BUN) and creatinine levels indicated hepatic and renal dysfunction. Blood was collected for the Microscopic Agglutination Test (MAT) and lipL32 rt-PCR, and urine was collected for lipL32 rt-PCR. Samples positive by lipL32 rt-PCR were genotyped by secY to identify the Leptospira species. Phylogeny of Leptospira spp. was based on secY gene sequence analysis using the Neighbor-Joining method. The evolutionary distances were computed using the Tamura-Nei method.

Result: Blood was negative by rt-PCR, but the MAT was positive for Pomona (1:6400). Urine was positive by rt-PCR and sequencing of secY amplicons presented 100% identity to L. interrogans. Phylogeny based secY gene sequence analysis revealed that the DNA from the dog urine clustered together with the reference strain of L. interrogans serovar Pomona and isolates from cattle in South America.

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