

TOPIC: Tick-borne Diseases (*Rickettsia*, *Ehrlichia*, *Borrelia*)

APPROACH: Vector-pathogen interaction

Distribution, transmission, and risk factors of infection with canine vector-borne pathogens in wild foxes and free-ranging dogs in Chile

Keywords: distribution; transmission; risk factors; canine pathogens; vector-borne; wild foxes; free-ranging dogs.

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Canine vector-borne pathogens (CVBP) distribution tends to be circumscribed to certain areas with climatic features where their vectors are able to persist. In this aspect, Chile possesses a marked variety of bioclimates that provides an ideal scenario to study the distribution of vector-borne pathogens, considering that ticks of the *Rhipicephalus sanguineus* species group are widely distributed in the country. Despite this, information about the presence, distribution, and impact of CVBP in domestic and wild canines in Chile is very scarce. In this study, blood and serum samples of 981 dogs, 155 Andean foxes (*Lycalopex culpaeus*), and 90 grey foxes (*L. griseus*) were obtained from six different bioclimatic regions throughout Chile. A set of primers and serological tests were used to detect presence or exposure of CVBP. Ticks retrieved were identified using taxonomic keys and molecular tools, and risk factors of infection were inferred. The occurrence *Anaplasma platys*, *Mycoplasma haemocanis*, and *Candidatus Mycoplasma haematoparvum* were confirmed in the three canid species and in all six bioclimatic regions with presence of *R. sanguineus*. *Ehrlichia canis* DNA was not detected in any sample. We also confirmed for the first time *Hepatozoon felis*, *H. americanum*, and *H. canis* in foxes of Chile. Finally, *Babesia vogeli* DNA and antibodies were found in dogs, while in foxes only antibodies against this agent were detected. No filariids other than *Acanthocheilonema reconditum*

were confirmed in our samples. Our molecular results support the hypothesis that interspecific transmission is taking place, and that free-ranging dogs in Chile could be favoring the maintenance of some CVBP in areas suitable for their tick vector. Due to the comprehensive nature of this work, in which the most relevant CVBP in canid species of Chile were studied across a latitudinal gradient of 3000 km, this project contributes to fill the knowledge gap in the epidemiology of vector-borne pathogens shared between domestic and wild animals, having implications in the transmission ways of the studied agents.