

CRYPTOSPORIDIUM AND GIARDIA IN MARINE WILDLIFE FROM THE INLAND WATERS OF WASHINGTON STATE

Joseph K. Gaydos*¹, Woutrina A. Miller¹, Kirsten V. K. Gilardi¹, Christine Kreuder-Johnson¹, Patricia Conrad¹, Ann Melli², Heather Zornetzer², Steven J. Jeffries³, Monique M. Lance³, and Chris Thompson⁴

¹ *UC Davis Wildlife Health Center, School of Veterinary Medicine, 1 Shields Ave., Davis, CA 95616*

² *Department of Pathology, Microbiology, and Immunology, UC Davis School of Veterinary Medicine, 1 Shields Ave. Davis, CA 95616*

³ *Washington Department of Fish and Wildlife, Marine Mammal Investigations, 7801 Phillips Rd. S.W., Tacoma, WA 98498*

⁴ *School of Aquatic & Fishery Sciences, Box 355020, University of Washington, Seattle, WA 98195*

ABSTRACT

Historically, *Cryptosporidium* and *Giardia* have been thought of as terrestrial and freshwater pathogens. Mounting evidence suggests that large amounts of feces being discharged, dumped, or carried in runoff into marine waters has now made these marine pathogens as well, however little is known about the epidemiology of these pathogens in marine wildlife. We tested harbor seals (*Phoca vitulina*), marine-foraging river otters (*Lontra canadensis*), and hybrid glaucous-winged / western gulls (*Larus glaucescens / occidentalis*), three common marine wildlife species in the Puget Sound region (Washington, USA), for infection with *Cryptosporidium* and *Giardia*. Fresh feces were collected from otter latrine sites and seal haul-out sites throughout the Puget Sound region. Gull fecal samples were collected from birds captured at sites proximal to sites where otters and seals were sampled. Samples were tested for *Cryptosporidium* and *Giardia* using ZnSO₄ floatation and immunomagnetic separation followed by direct immunofluorescence detection (IMS/DFA). Oocyst and cyst DNA was extracted, amplified using established primers, and compared to sequences of reference genotypes. *Giardia* cysts were detected in 4% of gull samples (n=78), 19% of river otter samples (n=57), and 43% of seal samples (n=99). Eleven positive seal samples were amplified by PCR and confirmed as *G. lamblia*. Three of the eleven sequences were from one site and were identified as the *G. lamblia* dog genotype, suggesting possible transmission to seals from wild canids, or more likely, domestic dogs. The sequences from the other eight samples represented a novel *G. lamblia* genotype. *Cryptosporidium* oocysts were detected in 7% of river otters sampled but not detected in gulls or seals. The one amplified otter sample was most similar to the ferret genotype of *C. parvum*. Marine wildlife shed *Cryptosporidium* and *Giardia* in the Puget Sound region but preliminary data failed to identify the genotypes most commonly infecting humans. In Puget Sound, seals, gulls, otters and other marine wildlife species frequent areas of shellfish farming and harvest. More work is needed to better understand the zoonotic potential of the novel genotypes identified as well as to better understand the impact of these pathogens on the wildlife species they infect.