

DETECTION OF INFLUENZAVIRUS MATRIX PROTEIN BY POLYMERASE CHAIN REACTION IN A NEONATAL HARBOR SEAL (*Phoca vitulina*) IN THE PACIFIC NORTHWEST

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ABSTRACT

Twenty-five years ago, the first outbreak of influenza A in non-human mammals was identified in a group of harbor seals and a pilot whale off the coast of Cape Cod, United States. Further investigation has since revealed both influenza A and B in a variety of other marine mammal species and in multiple regions worldwide. In addition, studies have shown that not only can both avian and human influenza viruses be transmitted to marine mammals, but that primitive strains of influenza B may someday have the potential for transmission from marine mammals back into the human population.

With a growing harbor seal population, increasing human-wildlife interactions, and an uncertain potential for both interspecies and zoonotic transmission, assessing the prevalence of influenza in marine mammal populations in order to mitigate the risk of exposure is essential. Since comprehensive evaluations of influenza antibody prevalence in wild seal populations remain limited, the goal of this study was to establish baseline information on the seroprevalence for influenza antibodies in harbor seals in the Pacific Northwest. In addition to determining the potential risk of human exposure and infection, documenting the seroprevalence of influenza is important from a population health perspective for harbor seals and other sympatric marine mammal species.

Serum samples, as well as oropharyngeal, nasal, and rectal swabs were collected from 43 neonatal harbor seals in Pacific Northwest rehabilitation facilities. No evidence of antibodies to avian influenza was detected. One of 43 pooled samples of nasal and oropharyngeal swabs was positive for influenza virus matrix protein by polymerase chain reaction. Failure to detect circulating antibodies may be related to the stage of immunologic development of the pup, incipient stage of infection, overall health status of this animal, and other factors. Additional molecular characterization disclosed that this sample represented neither group H7 nor H5, Asian and North American strains. Further molecular screening of the sample is underway. Despite detection of virus in only 1 animal, this study provides preliminary insights into a possible carrier host and illustrates the potential risk for human exposure to avian influenza virus at rehabilitation facilities.