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Phocine distemper virus in the North and European Seas – Data and models, nature and nurture

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ABSTRACT

Two outbreaks of phocine distemper have severely affected harbour seal (*Phoca vitulina*) populations in European and UK waters. The first occurred in 1988 when the causative virus was identified as a new member of the genus morbillivirus. The second outbreak in 2002 was first detected on the same Danish Island of Anholt and involved similar populations and geographical locations. However, despite the obvious similarities between the epidemics, differences in viral transmission and case mortality were found. Harbour seals are highly susceptible to infection while sympatric grey seals (*Halichoerus grypus*) are resistant but could be important asymptomatic carriers of the disease. Arctic phocid seals remain the most likely source of the virus and grey seals could be the link between these primary hosts and the harbour seal populations further south. Future epidemiological models should therefore consider including multiple host species. The future conservation and management of harbour seal populations vulnerable to PDV relies on the ability to accurately predict the long-term impact on population abundance and distribution. Although knowledge about the behaviour and pathogenesis of the virus has increased substantially and data on host movements and contact rates are accumulating, studies into the determinants of the host range have lagged behind. The development of more realistic epidemiological models should be combined with studies into the factors controlling species and individual susceptibility. Assessing the risk of infection to endangered but currently unexposed potential host species (such as the Hawaiian monk seal, *Monachus schauinslandi*) is essential for guiding potential conservation management options, such as vaccination.

1. Introduction

Phocine distemper virus (PDV) emerged as a devastating disease among harbour seals in Northern European and UK coastal waters in 1988 (Kennedy et al., 1988; Osterhaus and Vedder, 1988), causing catastrophic declines in many populations (Dietz et al., 1989; Hall et al., 1992a; Hall, 1995; Härkönen and Heide-Jørgensen, 1990; Heide-Jørgensen and Härkönen, 1992a). Over the six-month period beginning in April, more than 18,000 carcasses washed up along the shores of Europe and the UK (Fig. 1a, Dietz et al., 1989; Heide-Jørgensen et al., 1992b). PDV is a member of the genus morbillivirus within

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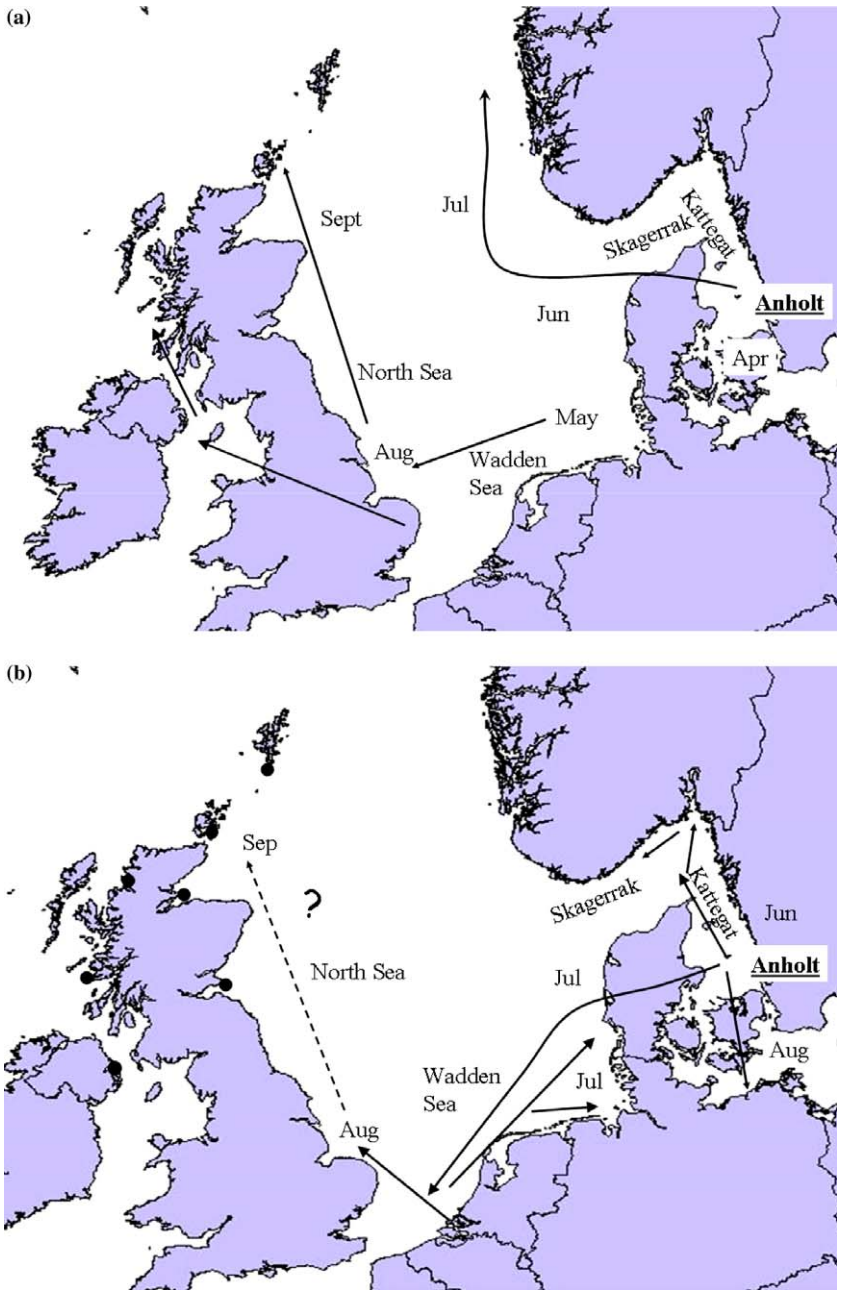

Fig. 1 – Maps showing the temporal and spatial spread of (a) the 1988 epidemic and (b) the 2002 epidemic from Anholt in the Kattegat to UK and Irish waters. The dotted line indicates that the disease did not reach epidemic proportions in Scotland or Northern Ireland, despite PDV seal deaths being found in many regions (shown by the black circles).

the *Paramyxoviridae* family that causes a severe respiratory and systemic infection in its host and has a high case fatality rate (Harder et al., 1990). In 2002 the disease re-emerged causing a second major outbreak (Jensen et al., 2002), affecting largely the same populations over a similar geographical area (Fig. 1b), with roughly the same epidemic duration and population impacts (more adult males than other sex-age groups were infected) (Härkönen et al., 2006). However, there were differences between the timing of the two epidemics and wide geographical variations in mortality rates. Comparing the two outbreaks may therefore provide important clues as to the nature, origin and enduring impact of the virus.

Information about the PDV virus itself has increased greatly over the last 17 years. The genes encoding for many of the major viral proteins have been sequenced (Curran et al., 1992; Curran et al., 1990; Curran and Rima, 1992; McIlhatton et al., 1997). Knowledge of the pathogenesis and aetiology of the disease and its potential sequelae has been obtained from detailed pathological studies of affected animals (Baker, 1992; Kennedy et al., 1989; Schumacher et al., 1990). However, information about the movements, distribution and population dynamics of its harbour seal host on a wide geographical scale have only recently been reported (Brasseur and Fedak, 2003; Härkönen et al., 1999; Ries et al., 1999).