

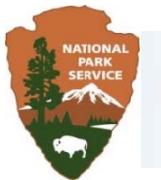
Wellfleet Bay Virus Workshop II

Tufts University

October 6, 2015



R. Mickley, USDA, APHIS WS



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Agenda

9:00 Welcome/Opening Remarks – Chris Dwyer

9:15 Wellfleet Bay Virus Genetics and Phylogenetics: An Overview and Update. Andrew B. Allison

9:45 Prevalence and Distribution of Wellfleet Bay Virus Exposure in the Common Eider (*Somateria mollissima*). Jennifer R. Ballard, Randall M. Mickley, Samantha E.J. Gibbs, Chris Dwyer, Catherine Soos, N. Jane Harms, H. Grant Gilchrist, Jeffrey S. Hall, J. Christian Franson, G. Randy Milton, Glen Parsons, Brad Allen, Jean-Francois Giroux, Stéphane Lair, Daniel G. Mead and John R. Fischer

10:15 Experimental Inoculation of the Common Eider (*Somateria mollissima*) With Wellfleet Bay Virus – A Comparison of Three Inoculation Routes. Jennifer R. Ballard, Daniel G. Mead, John R. Fischer and Valerie Shearn-Bochsler

10:45 Narrowing the focus of the Wellfleet Bay Virus Investigation: Annual Movement Patterns of Satellite-marked Common Eiders Breeding in Boston Harbor, MA. Lucas Savoy, Chris Dwyer, Randall M. Mickley, Samantha E.J. Gibbs, Glenn H. Olsen, H Heusmann, Susannah Corona and Jorge Ayub

11:15 An Investigation into the Potential Source Population of Common Eiders Found Dead at Jeremy Point via DNA Analysis. Sarah Sonsthagen, Chris Dwyer, Randall M. Mickley, Samantha E. J. Gibbs, Jean-Francois Giroux, Brad Allen and Randy Milton

11:45 Detection of Wellfleet Bay Virus Antibodies in Seabirds of the Northeastern United States. Jennifer R. Ballard, Randall M. Mickley, Justin D. Brown, NJ Hill, J.A. Runstadler, D. Clark, Daniel G. Mead, and John R. Fischer

Lunch 12:00 – 1:00

Management Implications (Informal Discussion or Presentations)

1:00 Perspectives from NPS and/or DCR on the Management of Boston Harbor Islands and Cape Cod National Seashore in Relation to Common Eiders and WFBV - Bob Cook, Jorge Ayub

1:20 Perspectives from MassWildlife on the Management & Conservation of Common Eiders in Massachusetts in Relation to WFBV - H Heusmann, Erik Amati

1:40 Perspectives from USFWS and USDA-WS on the Implications of WFBV to Common Eider Conservation & Management in the Northeastern U.S. – Chris Dwyer, Sam Gibbs, Randy Mickley, Jenn Ballard, Jenn Malpass

2:00 Panel Discussion – Ideas, Priorities and Next Steps

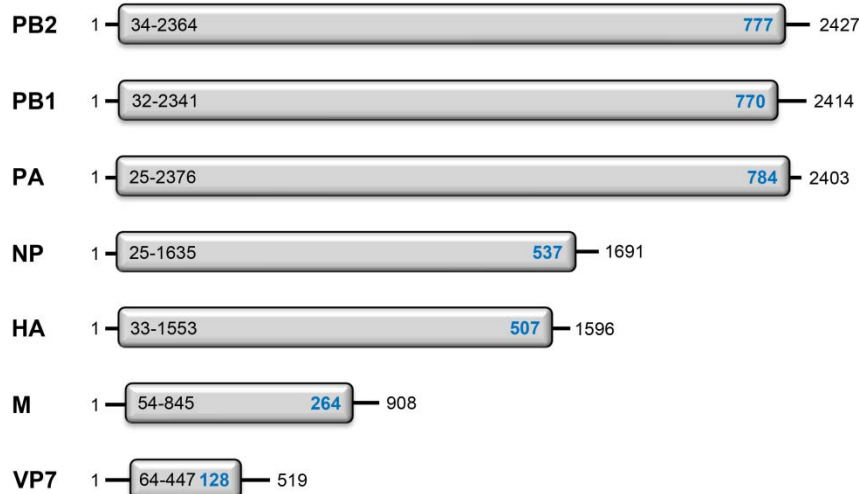
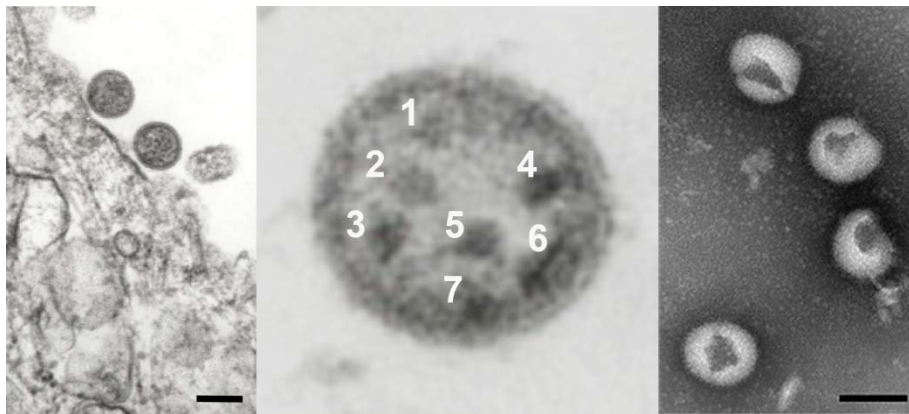
3:00 Special Recognitions and Torch Passing – Chris, Sam, Julie

Wellfleet Bay Virus Genetics and Phylogenetics: An Overview and Update

Andrew B. Allison, Baker Institute for Animal Health, Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, Ithaca, NY (aba75@cornell.edu)

ABSTRACT

Previously, we set out to characterize the genetic composition (RNA genome) of WFBV in order to determine its phylogenetic relationship to other orthomyxoviruses and tentatively deduce how the virus is being transmitted between eiders by analyzing its surface protein(s). Through such studies, we have been able to 1) determine the segmental configuration of the WFBV genome, 2) define the evolutionary relationship of WFBV to other orthomyxoviruses, in particular Cygnet River virus (CyRV) from South Australia, and 3) potentially discern insights into the mechanism of transmission by identifying the virus protein (surface receptor) used to infect cells. Such analyses have provided a baseline foundation for discerning additional epidemiological and ecological aspects of the virus, as well as to better understand the long-term implications it may have on common eider populations. In this report, I will provide an overview on what is currently known regarding the molecular biology of the virus and an update regarding the relationship of WFBV and CyRV, including a visit to the CyRV outbreak site in Kangaroo Island, South Australia.



Prevalence and Distribution of Wellfleet Bay Virus Exposure in the Common Eider (*Somateria mollissima*). Jennifer R. Ballard, Randall Mickley, Samantha E.J. Gibbs, Chris Dwyer, Catherine Soos, N. Jane Harms, H. Grant Gilchrist, Jeffrey S. Hall, J. Christian Franson, G. Randy Milton, Glen Parsons, Brad Allen, Jean-Francois Giroux, Stéphane Lair, Daniel G. Mead and John R. Fischer¹

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DGM - Southeastern Cooperative Wildlife Disease Study, Athens, Georgia

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ABSTRACT

Between 1998 and 2014, recurrent mortality events were reported in the American subspecies of the common eider (*Somateria mollissima dresseri*) on Cape Cod, Massachusetts near Wellfleet Harbor. The early die-offs were attributed to parasitism and emaciation, but beginning in 2006, a suite of distinct lesions was observed concomitant with the isolation of a previously unknown RNA virus. This novel pathogen was identified as an orthomyxovirus in the genus *Quaranjavirus*, and was named Wellfleet Bay virus (WFBV). To assess evidence of exposure to this virus in common eiders, a longitudinal study of the prevalence of WFBV antibodies at multiple locations was conducted. A total of 2,258 serum samples were collected between 2004 and 2014 from six locations and were analyzed using microneutralization assays. The results corroborate the emergence of WFBV in 2006 based on the first detection of antibodies in that year. Significantly higher seroprevalence was detected in the Massachusetts population of American common eiders compared to those in Maine, Nova Scotia, and Québec. Within the Massachusetts population, evidence of viral exposure varied by age, sex, and season of sampling, and prevalence by season and sex were highly interrelated, with greater numbers of seropositive males in the fall and females in the spring. No evidence of viral exposure was detected in the northern subspecies (*S.m. borealis*). Among the locations sampled, Massachusetts appears to be the epicenter of common eider exposure to WFBV. Further research is warranted to understand the factors controlling the epidemiology of WFBV at this location, including those that may be limiting expansion of its geographic range.

Experimental Inoculation of the Common Eider (*Somateria mollissima*) with Wellfleet Bay Virus – A Comparison of Three Inoculation Routes, Jennifer R. Ballard, Daniel G. Mead, John R. Fischer, Valerie Shearn-Bochsler

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ABSTRACT

Wellfleet Bay virus (WFBV) is an orthomyxovirus isolated from common eiders (*Somateria mollissima*) collected during recurrent mortality events on Cape Cod, Massachusetts. In this study, eider ducklings were inoculated with WFBV by oral, tracheal, and intradermal routes and observed for 30 days post inoculation (DPI). Sham-inoculated contact control birds were cohoused with each inoculation group, and a group of sham-inoculated control birds was housed separately. Oropharyngeal and cloacal swabs were collected from each bird every other day, and serum samples were collected weekly. Individuals from each group were euthanized at various time points from 2-30 DPI to examine tissue tropism of the virus and associated lesions. Only one bird demonstrated marked clinical disease, but inoculation by all three routes was associated with mild lethargy, anorexia, and stunted growth up to 5 DPI. Antibodies were detected after 7 DPI in the majority of exposed birds, regardless of the inoculation route. Gross and histologic lesions included hepatomegaly; pinpoint, pale foci on the liver; hepatocellular necrosis, splenic necrosis, exocrine pancreatic apoptosis, and lymphoid depletion of the spleen, thymus, and bursa. Virus was detected by virus isolation and nested, reverse transcription-polymerase chain reaction (RT-nPCR) in multiple tissues collected on or before 8 DPI, after which time lesions resolved and virus was not detected. Intermittent viral shedding was observed in inoculated birds prior to 8 DPI. No evidence of infection was detected in any of the control or contact control birds, based on negative serology, virus isolation, and RT-nPCR results from all samples. From these findings, it appears that WFBV can be experimentally transmitted by oral, tracheal, and intradermal routes, but clear differences between these routes are not apparent. Direct, bird-to-bird transmission did not occur. *Key words:* Wellfleet Bay virus, common eider, experimental inoculation



Narrowing the Focus of the Wellfleet Bay Virus Investigation: Annual Movement Patterns of Satellite-marked Common Eiders Breeding in Boston Harbor, MA. Lucas Savoy, Chris Dwyer, Randall M. Mickley, Samantha E.J. Gibbs, Glenn H. Olsen, H Heusmann, Susannah Corona, Jorge Ayub

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ABSTRACT

Between 1998 and 2011, 11 recognized mortality events occurred in Common Eiders (*Somateria mollissima*) along the coast of Cape Cod, Massachusetts, USA. The numbers of eiders involved in these outbreaks ranged from 30 to 2,800 individuals, with estimated total losses exceeding 6,000 birds. In 2010, a novel Orthomyxovirus named Wellfleet Bay Virus (WFBV) was isolated from the tissues of four of these birds.

In 2012, biologists accompanied crews visiting common eider nesting colonies in Massachusetts, Maine, Nova Scotia, and the Gulf of St. Lawrence to collect blood samples to screen for the presence of the WFBV. Results from this work suggest that eiders breeding in Boston Harbor had the greatest frequency of exposure to the virus among areas all sampled.

In the spring of 2013, we initiated a study to determine the annual movements of male and female eiders breeding in Boston Harbor. A total of 47 adult eiders were marked with satellite transmitters (12 in 2013, 19 in 2014, and 16 in 2015), and were intended to provide location data for 2.5 years. A total of 38 eiders have provided movement data. Molting locations varied, including areas of Maine, Massachusetts, Boston Harbor and the Gulf of St. Lawrence and Labrador, Canada. One of the marked birds died in November 2013, at the same location and time period as the eider WFBV die-off that season. Eiders wintered in three locations; Boston Harbor, Nantucket Sound area, and Long Island Sound. Data collected from this study provides a better understanding of the annual movements of eiders from a high virus outbreak area and their potential interactions with other Atlantic populations of eiders.



An Investigation into the Potential Source Population of Common Eiders Found Dead at Jeremy Point via DNA Analysis. Sarah Sonsthagen, [Chris Dwyer](#), Randall M. Mickley, Samantha E. J. Gibbs, Jean-Francois Giroux, Brad Allen and G. Randy Milton

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ABSTRACT

Recent mortality events of common eiders (*Somateria mollissima*) associated with the Wellfleet Bay virus (WFBV) on Cape Cod, MA, USA have led to questions regarding the geographic origin and potential population impacts (if any) of this disease on common eiders. Eiders that were previously banded in Maine, Nova Scotia and Quebec have been found dead on Cape Cod, although the limited number of recoveries continues to be insufficient for identifying the source population(s) of eiders affected. Given that the number of breeding common eiders associated with nearby Boston Harbor Islands has remained stable at approximately 300-5500 pairs, and mortality events have been approximately half that number annually, it was previously thought that a large segment of the eiders involved in these mortality events on Cape Cod were unlikely from the local population.

Common eiders are unique among sea ducks as they exhibit fine scale spatial genetic structure at both mitochondrial and nuclear markers. Thus, it may be possible to assign birds collected during the annual mortality events to breeding areas based on their genetic relatedness. This study is designed to develop a multi-locus data matrix containing reference samples from 7 breeding colonies sampled from Maine, Nova Scotia and the Gulf of St. Lawrence. Under a scenario of genetic structure among breeding colonies, we probabilistically assigned common eiders involved in annual mortality events to breeding areas using the data matrix to examine the spatial distribution and proportion of local and migratory birds involved in die off events on Cape Cod.

We collected genetic data from 12 microsatellite loci (Aph2, Aph8, Aph20, Aph23, Bca1, Cmo9, Sfi10, Smo4, Smo7, Smo8, Smo10, and Smo12) and 545 base pairs of mitochondrial DNA control region for eiders found dead during Fall 2013 and Spring 2014 (n = 221 total). We estimated indices of genetic diversity and tested for genetic differentiation among the seven breeding colonies with Arlequin. Common Eiders from Wellfleet Bay were assigned to breeding populations using the program Maximum Likelihood Classification (MLC). MLC provides maximum likelihood scores along with a probability of assignment of an individual to a breeding population. Of samples which had > 70% assignment probability (133/221), 28.5% matched reference samples from Boston Harbor, 51.1% matched reference samples from the Gulf of Maine (22.6% Maine; 28.5% Nova Scotia) and 20.3% matched reference samples from the Gulf of St. Lawrence. These results suggest that a high proportion of local eiders were involved in the 2013-14 dieoff's, which may be impacting eiders from the Gulf of Maine region more than other populations.

Detection of Wellfleet Bay Virus Antibodies in Seabirds of the Northeastern United States

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ABSTRACT

Wellfleet Bay virus is a recently described orthomyxovirus isolated from the tissues of common eiders (*Somateria mollissima*) collected during recurrent mortality events on Cape Cod, Massachusetts. A previous seroprevalence study in eiders, as well as the location of the recurrent mortality events, indicated that coastal Massachusetts is an epicenter of Wellfleet Bay virus exposure, but the reason for this is unknown. Opportunistic sampling of sympatric species and banked serum was used to investigate potential host range and spatiotemporal patterns of Wellfleet Bay virus exposure. Antibodies were detected in herring gulls (*Larus argentatus*), ring-billed gulls (*Larus delawarensis*), and two species of scoter (*Melanitta fusca* and *M. nigra*). These findings support the occurrence of fall/winter transmission and provide further insight into the host range epidemiology of Wellfleet Bay virus transmission in the northeastern United States.



We would like to thank the many individuals from the various agencies who participated in, volunteered or directly supported efforts to improve our understanding of the Wellfleet Bay Virus and common eiders. Our apologies to anyone who we may have missed...

H Heusmann –MADFW	Brian Bjorklund – USDA-WS
Dave Scarpitti – MADFW	Monte Chandler – USDA – WS
Erik Amati – MADFW	Justin Sypek – USDA – WS
Sue Ingalls – MADFW	Dave Warren – USDA - WS
Steve Wright - MADFW	Katie Brown – MADPH
Mike Huguenin - MADFW	Lauren Harris – USDA –VS
Lucas Savoy – BRI	Bob Brady – USDA – VS
Bill Hanson – BRI	Dan Berard – USDA – PPQ
Dustin Meattay – BRI	Justin Willey – USDA – PPQ
Robby Lambert – BRI	Keith Mueller – Coastal Bird Photography
Josh Beuth – RIDEM	Jack Golini – Capt. Jack Charters
Bob Cook – NPS	Russ Bowles – UMASS
Mary Hake - NPS	Michael Flanagan – Wellfleet Harbormaster
Jason Taylor – NPS	Leonard Croteau – Wellfleet Harbormaster
Marc Albert - NPS	David Rheault – Wellfleet Harbormaster
Susannah Corona – NPS	Ted Skiva – Wellfleet Harbormaster
Sheila Colwell – NPS	Chris Dwyer – USFWS
Nina Coleman – Town of Barnstable	Samantha Gibbs – USFWS
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Jennifer Taylor – Wildcare Rehabilitators	Scott Stipetich - USFWS
Stephanie Ellis – Wildcare Rehabilitators	Alex Dwyer – Volunteer
Charlie Tyler – MWRA	Scott Dwyer - Volunteer
Mike Delaney - MWRA	Ryan Dwyer - Volunteer
Glenn Olsen – USGS	Brad Allen - ME IF&W
Jorge Ayub – MA DCR	Kelsey Sullivan ME IF&W
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David Shaw – Univ. of GA	Carol Trocki, NPS Contractor
Michelle Kneeland – BRI	Christine Lepage, CWS
Virginia Stout – BRI	Justin Brown, UGA/SCWDS
Chris Kane – USFWS	
Jennifer Malpass – USFWS	
Randy Mickley – USDA – WS	

