SARS-CoV-2

The zoonosis from a human perspective

Eskild Petersen, MD, DMSc, DTM&H

Co-chair
ESCMID Emerging Infections Task Force
(European Society for Clinical Microbiology and Infectious Diseases)

Adjungated Professor
Institute for Clinical Medicine
Aarhus University
Denmark

Photo CDC
Intra- and inter species transmission of human Corona virus HCoV

Pathogenic coronavirus

Coronavirus in humans

Until 2020, six CoVs were known to infect humans, including human CoV 229E (HCoV-229E), HCoV-NL63, HCoV-OC43, HCoV-HKU1, SARS-CoV, and MERS-CoV. Although SARS-CoV and MERS-CoV have resulted in outbreaks with high mortality, others remain associated with mild upper-respiratory-tract illnesses.

There is a very big diversity of these [corona]viruses in the wild. We’ve been looking at bats ever since the SARS outbreak and bats are the real reservoir for SARS CoV.

And what we found is there’s this big diversity: we’ve found over 50 SARS-related coronaviruses in bats.

Peter Daszak
Two cats infected with SARS-CoV-2

While ACE2 receptor amino acid sequences in different animals show phylogenetic distance with respect to the human ACE2 receptor, the **pangolin**, **cat**, **felines**, and **dog** ACE2 receptor sequences cluster closely, and it predicts that the S protein of SARS-CoV-2 may bind to ACE2 in **domestic cats** and **dogs**, as well as a range of other species, including **pigs**, **cows**, **pangolins**, and **Chinese hamsters**.

FIGURE. Timeline of events related to SARS-CoV-2 infections in two domestic cats (cats A and B) kept as pets in two different households — New York, March 15–April 22, 2020

- Earliest respiratory illness onset in one of three ill persons in cat A household
- Symptom onset, cat A. Symptom onset, person in cat B household
- COVID-19 diagnosis, person in cat B household
- Resolution of symptoms in persons in cat A household (approximate)
- Resolution of cat B household member’s symptoms
- Cat A taken to veterinary clinic; received parenteral antibiotics. Specimens collected from cat A and sent to laboratory A
- Symptom onset, cat B
- Specimens collected from cat B sent to laboratory A
- Cat A recovered
- Cat B recovered
- Notification from laboratory A that cat A and cat B had positive results for SARS-CoV-2. Joint state and federal epidemiologic investigation began
- USDA NVSL confirmed SARS-CoV-2 infections; USDA and CDC issue joint announcement
- Additional specimens collected from cat A and cat B for confirmatory diagnosis at USDA NVSL

Month/Date
Mar 15 16 17 18 19 20 21 22
Apr 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
The mink most probably were infected by humans infected with SARS-CoV-2
All mammals have ACE2 receptors
2019-nCoV, SARS, MERS and pandemic H1N1

<table>
<thead>
<tr>
<th>Virus</th>
<th>Case Fatality Rate (%)</th>
<th>Pandemic</th>
<th>Contained</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>2019-nCoV</td>
<td>Unknown*</td>
<td>Unknown</td>
<td>No, efforts ongoing</td>
<td></td>
</tr>
<tr>
<td>pH1N1</td>
<td>0.02–0.4</td>
<td>Yes</td>
<td>No, postpandemic circulation and establishment in human population</td>
<td>Est. 200,000 deaths</td>
</tr>
<tr>
<td>H7N9</td>
<td>39</td>
<td>No</td>
<td>No, eradication efforts in poultry reservoir ongoing</td>
<td>No human to human transmission</td>
</tr>
<tr>
<td>NL63</td>
<td>Unknown</td>
<td>Unknown</td>
<td>No, endemic in human population</td>
<td></td>
</tr>
<tr>
<td>SARS-CoV</td>
<td>9.5</td>
<td>Yes</td>
<td>Yes, eradicated from intermediate animal reservoir</td>
<td>58% of cases result from nosocomial transmission</td>
</tr>
<tr>
<td>MERS-CoV</td>
<td>34.4</td>
<td>No</td>
<td>No, continuous circulation in animal reservoir and zoonotic spillover</td>
<td>70% of cases result from nosocomial transmission</td>
</tr>
<tr>
<td>Ebola virus (West Africa)</td>
<td>63</td>
<td>No</td>
<td>Yes</td>
<td></td>
</tr>
</tbody>
</table>

* Number will most likely continue to change until all infected persons recover.

A Novel Coronavirus Emerging in China - Key Questions for Impact Assessment

The 3rd February 2020
Comparing SARS-CoV-2 with SARS-CoV and influenza pandemics

Eskild Petersen, Marion Koopmans, Unyeong Go, Davidson H Hamer, Nicola Petrosillo, Francesco Castelli, Merete Storgaard, Sulien Al Khalili, Lone Simonsen

<table>
<thead>
<tr>
<th></th>
<th>Number of deaths (adjusted to year 2000 population)</th>
<th>Mean age at death (years)</th>
<th>Years of life lost (adjusted to year 2000 population)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2009 influenza pandemic</td>
<td>7500–44 100*; 8500–17 600†</td>
<td>37.4</td>
<td>334 000–1 973 000; 328 900–680 300</td>
</tr>
<tr>
<td>1968 influenza pandemic</td>
<td>86 000‡</td>
<td>62.2</td>
<td>1 693 000</td>
</tr>
<tr>
<td>1957 influenza pandemic</td>
<td>150 600‡</td>
<td>64.6</td>
<td>2 698 000</td>
</tr>
<tr>
<td>1918 influenza pandemic</td>
<td>1 272 300‡</td>
<td>27.2</td>
<td>63 718 000</td>
</tr>
<tr>
<td>1979–2001 average influenza A H3N2 season</td>
<td>47 800</td>
<td>75.7</td>
<td>594 000</td>
</tr>
<tr>
<td>2003 SARS-CoV</td>
<td>774</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>2012 MERS-CoV</td>
<td>858</td>
<td>&gt;65.0</td>
<td>Unknown</td>
</tr>
<tr>
<td>2019 SARS-CoV-2</td>
<td>302 059§</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

MERS-CoV = Middle East respiratory syndrome coronavirus. SARS-CoV = severe acute respiratory syndrome coronavirus. SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2. * Range based on estimates of excess pneumonia and influenza deaths (lower range number) and all-cause deaths (upper range number); estimated from projections of mortality surveillance from 122 cities. † Probabilistic estimates from the Centers for Disease Control and Prevention using 2009 pandemic survey data. ‡ Estimates based on the excess mortality approach applied to final national vital statistics and adjusted to year 2000 population-age structure. § As per the May 17, 2020, WHO situation report.

Table 3: Mortality from influenza and coronaviruses
The natural reservoir for influenzavirus is the intestine of birds.
New avian influenza A virus subtype combination H5N7 identified in Danish mallard ducks

K. Bragstad\textsuperscript{a}, P.H. Jørgensen\textsuperscript{b}, K.J. Handberg\textsuperscript{b}, S. Møller
gard\textsuperscript{c}, S. Corbet\textsuperscript{a}, A. Fomsgaard\textsuperscript{a,*}

\textsuperscript{a} Department of Virology, Statens Serum Institut, 5 Artillerivej, DK-2300 Copenhagen S, Denmark
\textsuperscript{b} Avian Virology, Danish Institute for Food and Veterinary Research, Department of Poultry, Fish and Fur Animals, Ministry of Food, Agriculture and Fisheries, Aarhus, Denmark
\textsuperscript{c} Danish Veterinary and Food Administration, Søborg, Denmark

Received 3 September 2004; received in revised form 13 December 2004; accepted 13 December 2004
Available online 30 January 2005

A recombinant avian influenza from a H7N7 outbreak in Italy in 1998 and a H5N2 from an outbreak in The Netherlands in 2001 surface in Denmark in 2003.

LPAI = Low Pathogenic Avian Influenza,

HPAI = High Pathogenic Avian Influenza
Human H7N9 cases since 2013

Tanner WD et al. Epidemiol Infect 2015;143:3359-74
H1N1 sw ("Classical")

1918 (avian source)

H1N1 sw-N Amer

H1N1 sw-Eurasian

Triple Reassortant Swine (2005-09)

230 cases (Ft Dix 1976)

Triple Reassort Sw + Eurasian Sw (2009)

11 cases

Pandemic H1N1

Seasonal H1N1

H1N1 hu extinct in 1957

H1N1 hu reintroduced in 1977

Don Burke, M.D. Dean, UPMC-Jonas Salk Chair in Global Health, Graduate School of Public Health, University of Pittsburgh - via ProMED
Incidence of ILI by age over selected 11 week epidemic periods in the UK

A short duration (1/σ3 = 40 weeks) of SARS-CoV-2 immunity could yield annual SARS-CoV-2 outbreaks. 
(B) Longer-term SARS-CoV-2 immunity (1/σ3 = 104 weeks) could yield biennial outbreaks, possibly with smaller outbreaks in the intervening years.

Projecting the Transmission Dynamics of SARS-CoV-2 Through the Postpandemic Period
In conclusion

SARS-CoV-2 like other CoV’s can infect humans and a broad range of mammals but has not been reported in birds.

This is not surprising given that the ACE2 receptor is found in all mammals with little genetic variation.

From a transmission point of view, SARS-CoV-2, has a high affinity for the human host like the human influenza’s.

Transmission between humans and mammals have been observed especially for mink and a few cases of dogs, cats and tigers.

The importance for the human epidemiology remain to be determined.