



Joint DANDRITE & iSEQ Seminar

Joint seminar between DANDRITE and the Centre for Integrative Sequencing (iSEQ)

Friday 3 October 2014 at 11.00 - 12.00

The Large Anatomy (building 1232, room 115)
Aarhus University, Wilhelm Meyers Allé, 8000 Aarhus C

Sandwiches in the ground area after the lecture (please sign up, see below)



Kristian Andersen

Harvard University
Broad Institute of MIT and Harvard

Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak

In its largest outbreak, Ebola virus disease is spreading through Guinea, Liberia, Sierra Leone, Nigeria, and Senegal with thousands of people infected.

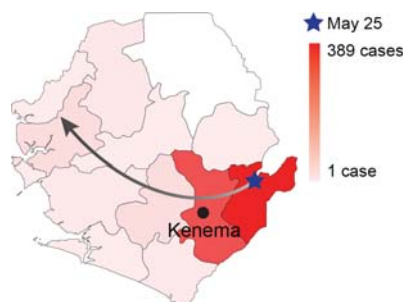
Our group sequenced 99 Ebola virus genomes from 78 patients in Sierra Leone to high depth of coverage. We found that the virus rapidly accumulates mutations inter- and intra-host, and we characterized patterns of viral transmission over the initial weeks of the epidemic. The West African variant likely diverged from central African lineages around 2004, crossed from Guinea to Sierra Leone in May 2014, and has exhibited sustained human-to-human transmission subsequently, with no evidence of additional zoonotic sources. Because many of the mutations alter protein sequences and other biologically meaningful targets, continued sequence-based monitoring as the outbreak progresses is critical to understand the impact of viral evolution on diagnostics, vaccines, and therapies.

Links:

<http://politiken.dk/viden/ECE2387911/ebola-jagten-paa-patient-zero-i-sierra-leone/>

<http://www.sciencemag.org/content/early/2014/08/27/science.1259657.full>

Host: Poul Nissen, Danish Research Institute of Translational Neuroscience - DANDRITE, Aarhus University



Sandwiches for participants in the ground area after the lecture.

Please email Anne Hedemand (anne@biomed.au.dk) no later than 1 Oct. 2014, if you would like to participate in the sandwich lunch (free but sign up needed).