

## DANDRITE Topical Seminar

Monday 10 April 2017 | 14.00-15.00

Jeppes Vontillius Auditorium - Bartholins Allé 3 – Building 1252, room 310



### Kristian G. Andersen

Assistant Professor | The Scripps Research Institute  
Member | Broad Institute of MIT and Harvard

### From Ebola to Zika – Tracking large-scale outbreaks using infectious disease genomics

The Ebola epidemic that ravaged West Africa from 2013 to 2016 was by far the largest outbreak of Ebola ever recorded. Weak healthcare infrastructure, overcrowded cities and community resistance to intervention allowed the epidemic to spin out of control. As the Ebola epidemic was winding down, another virus immediately took center stage - Zika. This virus had been causing multiple isolated epidemics since 2007, but was not recognized as a severe threat until it hit Brazil in 2015. It is now quickly spreading across the globe, causing a worldwide pandemic. Infectious disease outbreaks - such as those caused by Zika and Ebola - serve as stark reminders that emerging viruses pose one of the greatest threats to human health.

Our group is using viral genomics, computational biology, and traditional molecular biology, to gain insights into how viruses emerge and spread in human populations. By generating large-scale genomic datasets of Ebola virus sequences from hundred of infected patients, we dissected the trajectory of how Ebola rapidly spread across West Africa. More recently, our group sequenced and analyzed the first Zika virus dataset from local human transmissions and mosquitoes in Florida. Based on this data, we have been able to demonstrate that the Florida outbreak is much more complex than previously accepted. We show that multiple introductions happened into Florida in the spring of 2016 leading to sustained transmission chains. We show that these Zika virus lineages originated in the Caribbean and were likely brought to the United States via frequent cruise ship traffic. By modeling genomic data and mosquito abundance, we also show that Miami and Southern Florida is at particular risk for future Zika outbreaks.

**Host:** Core Group Leader and Director Poul Nissen, DANDRITE, Dept. of Molecular Biology and Genetics, Aarhus University

Relevant references:

Grubaugh et al. Multiple Introductions of Zika virus Into The United States Revealed Through Genomic Epidemiology bioRxiv doi: <https://doi.org/10.1101/104794> (2017).

Holmes et al. The Evolution of Ebola virus: Insights From the 2013-2016 Epidemic. *Nature* 538, 193-200 (2016).

Yozwiak et al. Roots, Not Parachutes: Research Collaborations Combat Outbreaks. *Cell* 166, 5-8 (2016).

Andersen et al. Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. *Cell* 162, 738-750 (2015).

Gire et al. Surveillance Elucidates Ebola virus Origin and Transmission During The 2014 Outbreak. *Science* 345, 1369-1372 (2014).