

# SFB 680

## MOLECULAR BASIS OF EVOLUTIONARY INNOVATIONS

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### **How viruses evolve and adapt**

Viruses are obligate parasites, needing hosts to survive, replicate and proliferate. Because of a high mutation rate and lack of error correction machinery, viral genomes evolve rapidly. Over time, they can become exquisitely adapted to specific hosts. However, spillovers between species are common. When such events occur, they can cause pandemics. As an example of this general theme, I will describe how the H1N1 Influenza A virus, which entered the human reservoir from birds, has adapted and evolved in humans since 1918. A study of viral sequences in humans shows that H1N1, while remaining highly infective, is evolving to become less visible to the immune system, thereby gradually coming to equilibrium (reducing its pathogenicity) in human hosts. It does so by changing the frequencies of certain sequence combinations in its RNA in a context dependent manner. Using oligonucleotides to infect dendritic cells, we showed that this effect can be traced to Toll-like receptors. As a second example, we will study the H5N1 virus, which caused a mini-pandemic a few years ago. This virus is also lethal in humans, but seems not to be transmissible between humans. A comparative study of H5N1 viral amino sequences in humans and birds shows that specific residues at loci on the HA protein are necessary for the virus to infect humans. We conjecture that these are necessary for the virus to attach efficiently to epithelial cells. Our study raises some interesting hypotheses about how to approach the study of emerging pandemics.

**June 19, 16:00**

**Institute for Genetics, Zölpicher Str. 47a, New Seminar Room, Ground Floor**

Host: Michael Lässig

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